

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1983	100.0	1983	6	AX469746	AX469746 Sequence
2	1928.6	97.3	2081	6	AX377796	AX377796 Sequence
3	1752	88.4	1752	6	AX469748	AX469748 Sequence
4	1459.4	73.6	2178	6	AX833215	AX833215 Sequence
5	1459.4	73.6	2178	9	AK094783	AK094783 Homo sapi
6	1073.2	54.1	2448	10	BC026374	BC026374 Mus muscu
7	1013	51.1	2456	6	AX375990	AX375990 Sequence
8	1013	51.1	2456	6	AX469751	AX469751 Sequence
9	1013	51.1	2456	9	AX358504	AX358504 Homo sapi
10	902	45.5	2178	6	AX377795	AX377795 Sequence
11	604.6	30.5	1602	4	AX921060	AX921060 Sequence
12	434.4	21.9	1985	4	AB094147	AB094147 Felis cat
13	431.8	21.8	1923	4	AB023629	AB023629 Canis fam
14	428.8	21.6	1717	4	AF036930	AF036930 Oryctolag
15	427.8	21.6	1975	9	BC012418	BC012418 Homo sapi
16	427.2	21.5	1717	6	BD137668	BD137668 Compositi
17	427.2	21.5	1893	9	AB010633	AB010633 Macaca fa
18	426.2	21.5	1966	6	AX329628	AX329628 Sequence
19	426.2	21.5	1966	6	AX409500	AX409500 Sequence
20	426.2	21.5	1966	9	HUMCOXYS	L07765 Human carbo
21	425.4	21.5	1976	4	AF064741	AF064741 Sus scrof
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24	419	21.1	1695	10	AF171640	AF171640 Rattus nor
25	417.4	21.0	1918	10	RATCHES	L46791 Rattus norv
26	415.8	21.0	1935	10	RNP161E	X51974 R. norvegicu
27	414.8	20.9	1766	9	HUMCARAA	M73499 Human carbo
28	414.8	20.9	1767	9	S73751	S73751 Homo sapien
29	414.8	20.9	1944	9	AF177775	AF177775 Homo sapi
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31	414.8	20.9	1958	9	AB119996	AB119996 Homo sapi
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33	412.6	20.8	1973	10	BC061789	BC061789 Rattus no
34	412.6	20.8	2141	6	AX401835	AX401835 Sequence
35	412.6	20.8	2141	10	RRESHVEL	X65296 R. rattus mR
36	411.6	20.8	1947	9	AY268104	AY268104 Homo sapi
37	409.4	20.6	1839	10	L81144	L81144 Rattus norv
38	405.2	20.4	1707	9	HSSE1	X52973 Homo sapien
39	399	20.1	1725	9	HUMCARBOX	M55509 Human liver
40	396	20.0	1868	10	D50578	D50578 Mesocricetu
41	395	19.9	1953	10	BC019198	BC019198 Mus muscu
42	395	19.9	1962	10	AF378751	AF378751 Mus muscu
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45	389.6	19.6	1885	10	RNU10697	U10697 Rattus norv

ALIGNMENTS

RESULT 1
AX469746
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX469746
Sequence 1 from Patent WO244357.
AX469746
AX469746.1 GI:21901868
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Kapeller-Libermann, R. and Silos-Santiago, I.
AUTHORS
METHODS
TITLE
JOURNAL
Methods of using 18903 to treat pain and pain-related disorders
Patent: WO 0244357-A 1 06-JUN-2002;
linear PAT 16-JUL-2002

OM nucleic - nucleic search, using sw model
Run on: August 11, 2004, 09:15:47 ; Search time 7739.27 Seconds
(without alignments)
11105.593 Million cell updates/sec
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Perfect score: 1983
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
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8: gb_pl:*
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Pred. No. is the number of results predicted by chance to have a


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AX377796
LOCUS AX377796 2081 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 29 from Patent WO0212467.
ACCESSION AX377796
VERSION AX377796.1 GI:19573887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Baughn, M.R., Bruns, C.M., Das, D., Deleage, A.M., Ding, L.,
Elliot, V.S., Gandhi, A.R., Griffin, J.A., Hafalia, A.J., Khan, F.A.,
Lal, P., Lee, S., Lu, D.A., Lu, Y., Patterson, C., Ramkumar, J.,
Ring, H.Z., Sanjanwala, M.S., Tang, Y.T., Thornton, M. and
Tribouley, C.M.
Drug metabolizing enzymes
Patent: WO 0212467-A 29 14-FEB-2002;
Incyte Genomics, Inc. (US)
FEATURES
source
1. 2081
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1931; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 18 CGAGGCTCCGCCCCAGTACTTGTCTGGCAGGATTAAGAGCAGATATAAGTGTGCTCAC 77
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Qy 198 TCTGCCCTGATGGCAGACGGCTTGGTGGCTTGGCTTGCACACCAAGAGCCCTCAAGTGTCA 257
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RESULT 4
LOCUS AX833215 2178 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 339 from Patent EP1347046.
ACCESSION AX833215
VERSION AX833215.1 GI:39919350
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and

Masuko, Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 339 24-SEP-2003;
Research Association for Biotechnology (JP)
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QY	1930	CCTGGGACACAGAGTCTTACCCA	1952
DB	1646	CCTGGGACACAGAGTCTTACCCA	1668
RESULT 6			
BC026374			
LOCUS			
DEFINITION	BC026374	2448 bp	mRNA linear ROD 06-OCT-2003
ACCESSION			Mus musculus cDNA sequence BC026374, mRNA (cDNA clone MGC:31116
VERSION			IMAGE:4163362), complete cds.
KEYWORDS	BC026374		BC026374
SOURCE			MGC.
ORGANISM			Mus musculus (house mouse)
REFERENCE			
AUTHORS			
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2448)
			Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F., Stachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.S., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Murray, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Matra, M.A.
TITLE			Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL			Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE			22388257
REFERENCE			12477932
AUTHORS			2 (bases 1 to 2448)
TITLE			Strausberg, R.
JOURNAL			Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK			NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT			Contact: MGC help desk Email: cgabbe@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES			
source			Location/Qualifiers 1..2448 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090"
			Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAP Plate: 43 Row: c Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22122766.

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Qy	1784	GAGAGAAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAAGACCTGAGAGCAGAGG	1843
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DEFINITION	AX469751		
ACCESSION	AX469751		
VERSION	AX469751.1	GI:21901872	
KEYWORDS			
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ORGANISM	Homo sapiens		
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AUTHORS	Kapeller-Libermann, R. and Silos-Santiago, I.		
TITLE	Methods of using 19903 to treat pain and pain-related disorders		
JOURNAL	Patent: WO 0244357-A 6 06-JUN-2002;		
FEATURES	Millennium Pharmaceuticals, Inc. (US)		
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complete cds.
ACCESSION AY358504
VERSION AY358504.1 GI:37182130
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2456)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wileand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL 12975309
PUBMED 2 (bases 1 to 2456)
REFERENCE Clark,H.F.
AUTHORS Direct Submission
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
JOURNAL Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
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ORIGIN
Query Match 51.1%; Score 1013; DB 9; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.5e-210;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;
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Db 388 GGTGCTTTGGCACACCAAGAGGCTCAAGTGTCAACCAATATGAACCTTCAAGGAAA 447
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DEFINITION Sequence 53 from Patent WO02068652.
ACCESSION AX921060
VERSION AX921060.1 GI:40214762
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Miyazaki, M., Sai, H., Taira, H. and Yamashita, T.
TITLE Nov-x proteins and nucleic acids encoding same
JOURNAL Patent: WO 02068652-A, 53, 06-SEP-2002;
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ORIGIN
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RESULT 12

AB094147

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AB094147 1995 bp mRNA linear MAM 22-APR-2003
Felis catus CES1 mRNA for carboxylesterase, complete cds.AB094147
AB094147.1 GI:30038512

Felis catus (cat)

Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

1 Miyazaki, M., Sai, H., Taira, H. and Yamashita, T.

Miyazaki, M., Sai, H., Taira, H. and Yamashita, T.

TITLE Molecular cloning of the feline liver carboxylesterase

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1985)
 AUTHORS Miyazaki,M., Sai,H., Taira,H. and Yamashita,T.
 TITLE Direct Submission
 JOURNAL Submitted (19-OCT-2002) Masao Miyazaki, Iwate University,
 Department of Agro-bioscience, Faculty of Agriculture, 3-18-8 Ueda,
 Morioka, Iwate 020-8550, Japan (E-mail:cdg83700@par.odn.ne.jp,
 Tel:81-19-621-6157, Fax:81-19-621-6177)
 FEATURES Location/Qualifiers

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ORIGIN

Query Match 21.9%; Score 434.4; DB 4; Length 1985;
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RESULT 13
 AB023629
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DEFINITION Canis familiaris CESD1 mRNA for carboxylesterase D1, complete cds.

ACCESSION AB023629
VERSION AB023629.1 GI:14331124
KEYWORDS carboxylesterase D1; Dog liver carboxylesterase D1.
SOURCE Canis familiaris (dog)

ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.

REFERENCE
1 (sites)
Hosokawa, M., Suzuki, K., Takahashi, D., Mori, M., Satoh, T. and
Chiba, K.

TITLE
Purification, molecular cloning, and functional expression of dog
liver microsomal acyl-CoA hydrolase: a member of the
carboxylesterase multigene family

JOURNAL Arch. Biochem. Biophys. 389 (2), 245-253 (2001)
MEDLINE 21237951
PubMed 11339814

REFERENCE
2 (bases 1 to 1923)
Hosokawa, M.

AUTHORS
Submitted (11-FEB-1999) Masakiyo Hosokawa, Chiba University,
Faculty of Pharmaceutical Sciences, 1-33 Yayoi-cho, Chiba, Chiba
263-8522, Japan (E-mail: masakiyo@p.chiba-u.ac.jp).
Tel: 81-43-290-2921, Fax: 81-43-290-2921)

FEATURES
Location/Qualifiers

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ORIGIN

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Best Local Similarity 56.5%; Pred. No. 1.6e-83;
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QY 434 CAGGAGTCT---CTGGGGCAGCTGGCTCGATGATAGTACGACGCGGGAACGGTACAAG 490
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DB 391 AAGAACAGCAGGCTGCGGCTGATGGTGTGATCCACGAGGGGGTCTGGTGGTGGCGGG 450

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RESULT 14
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 ACCESSION AF036930
 VERSION AF036930.1 GI:3219694
 KEYWORDS
 SOURCE
 ORGANISM Oryctolagus cuniculus (rabbit)
 Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1 (bases 1 to 1717)
 POTTER, P.M., PAWLIK, C.A., MORTON, C.L., NAEVE, C.W. and DANKS, M.K.
 Isolation and partial characterization of a cDNA encoding a rabbit
 liver carboxylesterase that activates the prodrug irinotecan
 (CPT-11)
 Cancer Res. 58 (12), 2646-2651 (1998)
 JOURNAL MEDLINE 98297515
 PUBMED 963592
 REFERENCE 2 (bases 1 to 1717)
 POTTER, P.M.
 Direct Submission
 Submitted (02-DEC-1997) Molecular Pharmacology, St. Jude Children's
 Research Hospital, 332 North Lauderdale, Memphis, TN 38105, USA
 JOURNAL
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 Query Match 21.68; Score 428.8; DB 4; Length 1717;
 Best Local Similarity 57.28; Pred No. 7.1e-83;
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RESULT 15
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 LOCUS
 DEFINITION Homo sapiens carboxylesterase 1 (monocyte/macrophage serine
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 cds.

ACCESSION BC012418
 VERSION BC01418.1 GI:15214584
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1975)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusi,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

TITLE
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 2398257
 PUBLISHED 12477932
 REFERENCE 2 (bases 1 to 1975)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/BTP/Gazdar
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
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 Series: IRAP Plate: 21 Row: m Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 16905523.

FEATURES

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Db	1108	GAATTAACACAGCAGGAGTTTGGCTGGTTGATTCAAATGTTTGTGATGAGCTATCCCACTCTCG	1167
Qy	1269	GGCAGGGCATGAGAAAGAAACCATCACTAAGATGCTCTGGAGTACCAGGACCCCTGTGTA	1328
Db	1168	AAGGCAACTGGACCAGAAACGACCATGTCTCTCTGTGGAAGTCTATCCCTTCTTT	1227
Qy	1329	ATATCAACAGGAGCAGGTACCACTTGTGTGGAGGAGTACTTGGAACAATGTCAATGAGC	1388
Db	1228	GCATTTGTATAGGAACCTGATTTCCAGAACCCACTGAGAAATACTTAGGAGGAACAGACGA	1287
Qy	1389	ATGACTTGAAGATGCTACGAAACCGTATGATGACATAGTTTCAAGATGCCACTTTCTGT	1448
Db	1288	CTGTCAAAAAGA-----AGACCTGTTCTTGAACCTTGATAGCAGATGTGATTTGGTG	1341
Qy	1449	ATGCCACACTGCAGACTGCTCACTACCAACGAGATGCCGCCCTCCCTGTCTACTCTGTATG	1508
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Qy	1509	AATTTGAGCACCAAGCTCG---TGGATATTCGTCAAAACCCGCACTGATGGGGCAGACC	1565
Db	1402	AGTTTTCAGTACCGTCCAAGCTTCTCATCAGACATGAAACCCACAGACGGTGATAGGAGACC	1461
Qy	1566	ATGGGATGAGATGTACTTCTCTTTTGGGGGCCCTTTCCGCCACAGGGCTTTCCATGGGTA	1625

Db	1462	ACGGGGATGAGCTCTTCTCCGCTCTTTGGGGCCCATTTTTAAAGAGGGTGCCCTCAGAAG	1521
Qy	1626	AGGAGAAGGCACCTTAGCTCCAGATGATGAAATACTGGGCCAACTTTGCCGCCACACAGGAA	1685
Db	1522	AGGAGATCAGACCTTAGCAAGATGGTGATGAAATCTGGGCCAACTTTGCTCGCAATGGAA	1581
Qy	1686	ACCCCAATGATGGGAATCTGCCCTGCTGGGCCACGCTACACACAGGATGAAAAGTACTCTGC	1745
Db	1582	ACCCCAATGGGGAAGGGCTCCGCCACTGGGCCAGGTACACCCAGGAAGGAAGGTACTCTGC	1641
Qy	1746	AGCTGGATTTTACCACAAGAGTGGGCGATGAAGCTCAAGGAGAAGAGATGGCTTTTGTGA	1805
Db	1642	AGATTGGTGCCACACCCAGCGCGCCAGAGCTGAGGACAAAGAGTAGCTTCTCTGGA	1701
Qy	1806	TGAGTGTGT	1814
Db	1702	CCAACTCT	1710

Search completed: August 11, 2004, 15:29:42
Job time : 7763.27 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 09:13:52 ; Search time 780.458 Seconds
(without alignments)
10793.891 Million cell updates/sec

Title: US-10-001-227-1
Perfect score: 1983
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 337363 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1983	100.0	1983	6	ABN84189 Human car
2	1928.6	97.3	2081	6	AD333489 Human dru
3	1271.8	64.1	1532	5	AA574822 DNA encod
4	1013	51.1	2456	2	AZ34105 Human PRO
5	1013	51.1	2456	3	AAZ34105 Human PRO
6	1013	51.1	2456	4	AA545953 Human DNA
7	1013	51.1	2456	7	ABx78556 Human PRO
8	1013	51.1	2456	7	ACA75528 Novel hum
9	1013	51.1	2456	7	ACA71008 Human sec
10	1013	51.1	2456	7	ACC87536 Human sec
11	1013	51.1	2456	7	ACC86922 Human sec
12	1013	51.1	2456	7	ACD04095 Human sec
13	1013	51.1	2456	7	ACA69426 CDNA enco
14	1013	51.1	2456	7	ACA90271 Novel hum
15	1013	51.1	2456	7	ACC89378 Human sec
16	1013	51.1	2456	7	ACA98169 Novel hum
17	1013	51.1	2456	7	ACA93811 Human sec
18	1013	51.1	2456	7	ACD15204 Human sec
19	1013	51.1	2456	7	ACD08791 Human sec
20	1013	51.1	2456	7	ACC98711 Human sec
21	1013	51.1	2456	7	ACF15432 Human sec
22	1013	51.1	2456	7	ACD42638 Novel hum
23	1013	51.1	2456	7	ACA72799 Human PRO

24	1013	51.1	2456	7	ACD02971	Novel hum
25	1013	51.1	2456	7	ACD01786	Novel hum
26	1013	51.1	2456	7	ACA91978	Novel hum
27	1013	51.1	2456	7	ACA63673	Novel hum
28	1013	51.1	2456	7	ACA89403	CDNA enco
29	1013	51.1	2456	7	ACA73413	Human sec
30	1013	51.1	2456	7	ACA05728	Human sec
31	1013	51.1	2456	7	ACA66562	CDNA enco
32	1013	51.1	2456	7	ACF20137	Human sec
33	1013	51.1	2456	7	ACF19523	Human sec
34	1013	51.1	2456	7	ACD21811	Human sec
35	1013	51.1	2456	7	ACF12976	Human sec
36	1013	51.1	2456	7	ACD25079	Human sec
37	1013	51.1	2456	7	ACF00128	Human sec
38	1013	51.1	2456	7	ACA72185	Novel hum
39	1013	51.1	2456	7	ACD04709	Novel hum
40	1013	51.1	2456	7	ACD18170	Human sec
41	1013	51.1	2456	7	ACD08177	Human sec
42	1013	51.1	2456	7	ACA88611	Novel hum
43	1013	51.1	2456	7	ACA70053	Human sec
44	1013	51.1	2456	7	ACD12275	Novel hum
45	1013	51.1	2456	7	ACC74190	Human sec

ALIGNMENTS

RESULT 1

ABN84189
ID ABN84189 standard; CDNA; 1983 BP.

AC ABN84189;

DT 23-SEP-2002 (first entry)

DE Human carboxylesterase-2 cDNA.

XX Carboxylesterase-2; COE-2; human; antiinflammatory; virucide; antiulcer;
KW antiasthmatic; antirheumatic; antiarthritic; dermatological;
KW antipsoriatic; analgesic; antitumour; cytostatic; enzyme; gene therapy;
KW gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 98..1852

FT /tag= a

FT /product= "Carboxylesterase-2"

FT /note= "the CDS is also specifically claimed in Claim 1"

XX WO200244357-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-US045356.

XX 30-NOV-2000; 2000US-0250929P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Kapeller-Libermann R, Silos-Santiago I;

XX WPI; 2002-537452/57.

XX P-PSDB; AB579484.

XX Novel isolated human carboxylesterase-2 family member polypeptide, 18903,
PT useful for treating inflammatory disorders, pain disorders, tumor and
cancer.

XX Claim 1; Page 119-122; 129pp; English.

XX The present sequence, the coding region of which is also claimed, is that
CC of human CDNA clone Fb18903, which encodes carboxylesterase-2 (COE-2,

see ABB79484), a novel carboxylesterase family member. COB-2 participates in the metabolism of various lipid and fatty acid compounds which are involved in pain and/or inflammation signalling. It is highly expressed in tissues which contain afferent neurons, particularly brain and spinal cord tissue. The invention provides COB-2 nucleic acid molecules, host cells, transgenic animals, isolated COB-2 proteins, fusion proteins, antisense nucleic acid molecules, recombinant expression vectors, host cells, transgenic animals, isolated COB-2 proteins, fusion proteins, used in claimed methods of identifying subjects having, or at risk of developing, an inflammatory or pain disorder. Compounds capable of treating an inflammatory or pain disorder can be identified from their ability to modulate COB-2 nucleic acid expression or COB-2 polypeptide activity. Modulator compounds are used in a claimed method of treating an inflammatory or pain disorder. Carboxylesterase-associated pain disorders include hyperalgesia, pain associated with musculoskeletal disorders and pain associated with surgery, rheumatoid arthritis, viral infection, allergic reaction, asthma, pancreatitis, somatoform disorders, fibromyalgia syndrome, etc. Carboxylesterase-associated inflammatory disorders include viral infection, ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis, scleroderma, psoriasis, inflammatory bowel disorder, peritonitis, chronic obstructive pulmonary disease, lung inflammation, asthma, appendicitis, septic shock, nephritis, amyloidosis, chronic bronchitis, sarcoidosis, scleroderma, lupus, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, inflammatory breast disease, orbital inflammatory disease. Other carboxylesterase-associated disorders include tumours, cancer, aberrant blood pressure, aberrant blood clotting, misregulation of various reproductive functions e.g. induction of labour, and misregulation of the sleep/wake cycle. COB-2 nucleic acids and polypeptides are also useful in screening assays, detection assays (e.g., chromosomal mapping, tissue typing, forensic biology) and predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics)

Sequence 1983 BP; 460 A; 553 C; 561 G; 409 T; 0 U; 0 Other;

Query Match	Best Local Similarity	100.0%	Score 1983;	DB 6;	Length 1983;
Marches 1983;	Conservative	0;	Mismatches	0;	Indels
0;	0;	0;	Gaps	0;	
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Dy 1	1	1	1	1	1
Qy 61	61	61	61	61	61
Dy 61	61	61	61	61	61
Qy 121	121	121	121	121	121
Dy 121	121	121	121	121	121
Qy 181	181	181	181	181	181
Dy 181	181	181	181	181	181
Qy 241	241	241	241	241	241
Dy 241	241	241	241	241	241
Qy 301	301	301	301	301	301
Dy 301	301	301	301	301	301
Qy 361	361	361	361	361	361
Dy 361	361	361	361	361	361
Qy 421	421	421	421	421	421
Dy 421	421	421	421	421	421
Qy 481	481	481	481	481	481
Dy 481	481	481	481	481	481

481	ACGGTACAAGTGGCTGGCTTTCAGCGAGGACTGTCTGTACCTGAACCTGACGCGCGGC	540
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541	GCGCGCGCGCGGGATCCAGCTGCCAGTGGTCTGGTTCGGGAGGCGGCTTCAT	600
601	CGTGGCGGCTCTCTTCGTACGAGGCTCTGACTTGGCGCGCGGAGAAAGTGGTCT	660
601	CGTGGCGGCTCTCTTCGTACGAGGCTCTGACTTGGCGCGCGGAGAAAGTGGTCT	660
661	GGTGTTCGAGCAGCAGGCTCGGCATCTTCGGCTTCCTGAGCAGCAGCAGCAGCAGC	720
661	GGTGTTCGAGCAGCAGGCTCGGCATCTTCGGCTTCCTGAGCAGCAGCAGCAGCAGC	720
721	GCGCGGGAACCTGGGGGCTGTGACACAGATGGGGCTCTCGCTGGGTGAGGAGAACAT	780
721	GCGCGGGAACCTGGGGGCTGTGACACAGATGGGGCTCTCGCTGGGTGAGGAGAACAT	780
781	GCGAGCCTTCGGGGAGACCCAGGAAATGTACCTTCCTGGGCTTCGGGGGGCCAT	840
781	GCGAGCCTTCGGGGAGACCCAGGAAATGTACCTTCCTGGGCTTCGGGGGGCCAT	840
841	GAGCATCTCAGGACTGATGTACACCCCTAGCCTCGGCTCTCTTCATCGGGCCATTTTC	900
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901	CCAGAGTGGACCCGGTATTTCAGATTTTCATCTAGTAACTCCACTGAAAGTGGCAA	960
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961	GAAGTGGCCACCTGGTGTGATGCAACCAACAGCAGCAGATCTCTGTAAGTGCCT	1020
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1021	GAGGCACTATCAGGACCAAGGTGATGCGTGTGTCCAAAGATGAGATTCCTCAACT	1080
1081	GAACTTCAGAGACCCGGAGAGATTATCTGGTCCATGAGCCCTGTGGTGGTGTGT	1140
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1321	CTGTGTGAATATCAAGAGAGAGGTACCATTTGGTGGAGAGTACCTGACATGT	1380
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1561	AGACCATGGGATGAGATGTACTTCTTTGGGGGCCCTTCGACACAGGCTTTCCAT	1620
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QY 1621 GGTAAGGAGGACCTTTAGCCTCCAGATGATGAATACTGGGCCAACTTTGGCCGCAC 1680
DB 1621 GGTAAGGAGGACCTTTAGCCTCCAGATGATGAATACTGGGCCAACTTTGGCCGCAC 1680
QY 1681 AGGAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACCAAGGATGAAAGTA 1740
DB 1681 AGGAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACCAAGGATGAAAGTA 1740
QY 1741 CTGACAGTGGATTTTACCAACAGAGTGGGATGAAGCTCAAGGAGAAAGATGCTTT 1800
DB 1741 CTGACAGTGGATTTTACCAACAGAGTGGGATGAAGCTCAAGGAGAAAGATGCTTT 1800
QY 1801 TTGGATGAGTCTTACAGTCTCAAGACTCAAGAGCTGAGAGAGAGCAATTTAAGGTGGCT 1860
DB 1801 TTGGATGAGTCTTACAGTCTCAAGACTCAAGAGCTGAGAGAGAGCAATTTAAGGTGGCT 1860
QY 1861 ATCCAGGAGGAGCCAAAGAGGGTTTGGCCCAACATCCAGCCCTGGGGAGCTAGCC 1920
DB 1861 ATCCAGGAGGAGCCAAAGAGGGTTTGGCCCAACATCCAGCCCTGGGGAGCTAGCC 1920
QY 1921 ATCGACATACCTCGGACAGAGTCTTACCCAGGCGAATTCGTTTAAACCTGCAGGAC 1980
DB 1921 ATCGACATACCTCGGACAGAGTCTTACCCAGGCGAATTCGTTTAAACCTGCAGGAC 1980
QY 1981 TAG 1983
DB 1981 TAG 1983

RESULT 2
AAD33489
ID AAD33489 standard; cDNA; 2081 BP.
AC AAD33489;
XX
DT 01-JUL-2002 (first entry)
DE Human drug metabolising enzyme (DME-10) cDNA.
XX Human; drug metabolising enzyme; cell proliferative disorder; metabolic;
KW autoimmune; inflammatory; developmental; gastrointestinal; hypergonadal;
KW pancreatic; endocrine; eye; dermatitis; Addison's disease; antilipemic;
KW acquired immunodeficiency syndrome; AIDS; glomerulonephritis; anorectic;
KW diabetes; atherosclerosis; adult respiratory distress syndrome; anaemia;
KW Grave's disease; thyroiditis; Crohn's disease; infection; anticoagulant;
KW systemic lupus erythematosus; cirrhosis; psoriasis; epilepsy; gastritis;
KW cataract; hypopituitarism; cancer; rheumatoid arthritis; conjunctivitis;
KW cystic fibrosis; peptic ulcer; Wilson's disease; hepatitis; antithyroid;
KW allergy; diarrhoea; thrombosis; obesity; immunostimulant; tranquilizer;
KW infertility; vulnery; anticonvulsant; gynaecological; laxative; goitre;
KW nontropic; jaundice; trauma; asthma; DME-10; enzyme; gene; ss.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 107..1861
FT /*tag= a
FT /product= "Human DME-10"
FT sig_peptide 107..235
FT /*tag= b
FT mat_peptide 236..1858
FT /*tag= c
FT /product= "Mature human DME-10 protein"
XX WO200212467-A2.
XX
XX 14-FEB-2002.
XX
XX 03-AUG-2001; 2001WO-US024382.
XX
XX 04-AUG-2000; 2000US-0223055P.
XX
PR 11-AUG-2000; 2000US-0224728P.

PR 18-AUG-2000; 2000US-0226440P.
PR 24-AUG-2000; 2000US-0228067P.
PR 31-AUG-2000; 2000US-0230063P.
PR 13-SEP-2000; 2000US-0232244P.
PR 20-SEP-2000; 2000US-0234269P.
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Baughn MR, Bruns CM, Das D, Delegeane AM, Ding L, Elliot VS,
PI Gandhi AR, Griffin JA, Hafalia AJA, Khan FA, Lal P, Lee S, Lu DM,
PI Lu Y, Patterson C, Ramkumar J, Ring HZ, Sanjanwala MS, Tang YT,
PI Thangavelu K, Thornton M, Tribouley CM, Walia NK, Warren BR, Yang J,
PI Yao MG, Yue H;
XX WPI; 2002-206331/26.
DR P-PSDB; AAE21052.
XX
PT New human drug metabolizing enzyme polypeptide and polynucleotide useful
PT for diagnosing, treating and preventing cell proliferative,
PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
PT disorders.
XX
PS Claim 73; Page 172; 179pp; English.

CC The invention relates to an isolated human drug metabolising enzyme (DME)
CC polypeptide or a biologically active or immunogenic fragment of DME. DME
CC is useful for diagnosis, treatment and prevention of cell proliferative,
CC autoimmune/inflammatory, developmental, endocrine, eye, metabolic and
CC gastrointestinal disorders including liver disorders. Autoimmune/
CC inflammatory disorders include acquired immunodeficiency syndrome (AIDS),
CC adult respiratory distress syndrome, Addison's disease, atherosclerosis,
CC allergies, anaemia, asthma, autoimmune haemolytic anaemia, diabetes mellitus,
CC thyroiditis, Crohn's disease, atopic dermatitis, diabetes mellitus,
CC glomerulonephritis, rheumatoid arthritis, systemic lupus erythematosus,
CC ulcerative colitis, uveitis, viral, bacterial, protozoal, parasitic,
CC fungal, helminthic infections and trauma. Cell proliferative disorders
CC include cancer, arteriosclerosis, cirrhosis and psoriasis; developmental
CC disorders include epilepsy and cataract; and endocrine disorders include
CC disorders of hypothalamus/pituitary, disorders associated with
CC hypopituitarism including diabetes insipidus, hypogonadism, disorders
CC associated with hypothyroidism including goitre, Grave's disease,
CC pancreatic disorders such as diabetes mellitus, disorders associated with
CC adrenals, disorders associated with gonadal steroid hormones such as
CC endometriosis, infertility, hypergonadal disorders and gynaecomastia.
CC Disorders of the eye include conjunctivitis and macular degeneration and
CC metabolic disorders include diabetes, cystic fibrosis, obesity and
CC hypocalcaemia. Gastrointestinal disorders include gastritis, peptic
CC ulcer, hepatitis, constipation, diarrhoea, jaundice, Wilson's disease,
CC thrombosis and hepatic tumours. DME gene is useful in gene therapy. The
CC present sequence is human DME-10 cDNA

XX Sequence 2081 BP; 473 A; 589 C; 583 G; 436 T; 0 U; 0 Other;

Query Match 97.3%; Score 1928.6; DB 6; Length 2081;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1931; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DB 27 CAATTCCCGCCCCAGTACTTGTGGCAGGATTAAAGACAGATAAAAGTGTGCTAC 86
QY 78 ACATGTAGACACGGCTACCATGCCATCCACAGTGTGCCATCCACAGTGTGCTAC 137
DB 87 ACATGTAGACACGGCTACCATGCCATCCACAGTGTGCCATCCACAGTGTGCTAC 146
QY 138 TCCTGCCACACAGGAGCTGGCTGGAGCATGAGTGTGATTTCTGCTGGAGCTCACCC 197
DB 147 TCCTGCCACACAGGAGCTGGCTGGAGCATGAGTGTGATTTCTGCTGGAGCTCACCC 206
QY 198 TCTGCTGATGCGCAGACGGCTTGGGTGCTTGCACACCAAGAGGCTCAAGTGTGCA 257
DB 207 TCTGCTGATGCGCAGACGGCTTGGGTGCTTGCACACCAAGAGGCTCAAGTGTGCA 266

QY 258 CCAATATGGAACCTTCAAGGAAACAGATGATGTGGGGAAGACACCCATCCAAAGTCT 317
Db 267 CCAATATGGAACCTTCAAGGAAACAGATGATGTGGGGAAGACACCCATCCAAAGTCT 326
QY 318 TTTTGGAGTCCCTTCTCAGACCTCTCTAGGTATCCTCAGGTTTGCACCTCCAGAAC 377
Db 327 TTTTGGAGTCCCTTCTCAGACCTCTCTAGGTATCCTCAGGTTTGCACCTCCAGAAC 386
QY 378 CCCGGAGCCCTGGAAGGAATCAGAGATCTACACCTACCCGCTGGTGCCTGCAGG 437
Db 387 CCCGGAGCCCTGGAAGGAATCAGAGATCTACACCTACCCGCTGGTGCCTGCAGG 446
QY 438 AGTCCTGGGCGAGCTGGCTCAGATGATAGTACGACGCGGGAACCGTACAGTGGCTGC 497
Db 447 AGTCCTGGGCGAGCTGGCTCAGATGATAGTACGACGCGGGAACCGTACAGTGGCTGC 506
QY 498 GCTTCAGCGAGGACTGCTGTACTGAACGTGTACGCGCGCGCGCGCGCGCGCGGATC 557
Db 507 GCTTCAGCGAGGACTGCTGTACTGAACGTGTACGCGCGCGCGCGCGCGCGCGGATC 566
QY 558 CCAGCTGCCAGTGAATGCTGTGTTCCGGGAGCGCGCTTTCATCGTGGGCGCTGCTTCTT 617
Db 567 CCAGCTGCCAGTGAATGCTGTGTTCCGGGAGCGCGCTTTCATCGTGGGCGCTGCTTCTT 626
QY 618 CGTACAGGAGCTCTGACTTGGCGCGCGCGGAGAAAGTGTGTGTGTCTTCGACGACA 677
Db 627 CGTACAGGAGCTCTGACTTGGCGCGCGCGGAGAAAGTGTGTGTGTCTTCGACGACA 686
QY 678 GGCTTCGCACTTTCGGCTTCTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 737
Db 687 GGCTTCGCACTTTCGGCTTCTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 746
QY 738 TGCTTGGACAGATGGCGCTCTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 797
Db 747 TGCTTGGACAGATGGCGCTCTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 806
QY 798 ACCAGGAAATGTGACCTGTTTCGGCCAGTGGCGGGGGCCATGAGCATCTCAGACCTGA 857
Db 807 ACCAGGAAATGTGACCTGTTTCGGCCAGTGGCGGGGGCCATGAGCATCTCAGACCTGA 866
QY 858 TGATGTCAACCTTAGCTCCGGTCTCTTCATCGGGCCATTTCCAGAGTGGCACCGGCT 917
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Db 1347 AGGAGCAGGTACCACTTGTGGTGGAGGATACCTGGACAAATGTCAATGAGCATGACTGGA 1406
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QY 1578 TGTACTTCTCTTGTGGGGCCCTTTCGCCACAGCGCTTTCCATGGGTAGGAGAAAGGCAC 1637
Db 1587 TGTACTTCTCTTGTGGGGCCCTTTCGCCACAGCGCTTTCCATGGGTAGGAGAAAGGCAC 1646
QY 1638 TTRGCTCCAGATGATGAATACTTGGCCCAACTTTGCCCGCACAGGAAACCCCAATGATG 1697
Db 1647 TTRGCTCCAGATGATGAATACTTGGCCCAACTTTGCCCGCACAGGAAACCCCAATGATG 1706
QY 1698 GGAATCTGCCCTGTGGCCACGCTTACAAAGGATGAAAGTACCTGCAGCTGGATTTTA 1757
Db 1707 GGAATCTGCCCTGTGGCCACGCTTACAAAGGATGAAAGTACCTGCAGCTGGATTTTA 1766
QY 1758 CCAGAGTGGGATGAAGTCAAGGAGAGAGATGGCTTTTGGATGAGTCTGTACC 1817
Db 1767 CCAGAGTGGGATGAAGTCAAGGAGAGAGATGGCTTTTGGATGAGTCTGTACC 1826
QY 1818 AGTCTCAAGACCTGAGAGCAGAGGCAATTTCTAAGGGTGGCTATGAGGAGAGGCCAA 1877
Db 1827 AGTCTCAAGACCTGAGAGCAGAGGCAATTTCTAAGGGTGGCTATGAGGAGAGGCCAA 1886
QY 1878 AGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1937
Db 1887 AGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1946
QY 1938 CAAGAGTTCTACCCA 1952
Db 1947 CAAGAGTTCTACCCA 1961
RESULT 3
AAS74822
ID AAS74822 standard; cDNA; 1532 BP.
XX AAS74822;
AC AAS74822;
XX XX
DT 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #10626.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS WO200175067-A2.
XX PN 11-OCT-2001.
XX PD 30-MAR-2001; 2001WO-US008631.
XX PF 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00549167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR

AC AAZ34105;
 XX 07-DEC-1999 (first entry)
 XX Human PRO873 nucleotide sequence.
 DE
 XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein; ss.
 XX
 OS Homo sapiens.
 FN WO9946281-A2.
 XX
 XX 16-SEP-1999.
 XX 08-MAR-1999; 99WO-US005028.
 XX
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00804020.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0079294P.
 PR 25-MAR-1998; 98US-0079856P.
 PR 26-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080332P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 09-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081209P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 23-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082767P.
 PR 23-APR-1998; 98US-0082796P.
 PR 27-APR-1998; 98US-0083336P.
 PR 28-APR-1998; 98US-0083322P.
 PR 29-APR-1998; 98US-0083392P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 29-APR-1998; 98US-0083500P.
 PR 29-APR-1998; 98US-0083545P.
 PR 29-APR-1998; 98US-0083554P.
 PR 29-APR-1998; 98US-0083558P.

PR 29-APR-1998; 98US-0083559P.
 PR 30-APR-1998; 98US-0083742P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 06-MAY-1998; 98US-0084441P.
 PR 07-MAY-1998; 98US-0084598P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 07-MAY-1998; 98US-0084627P.
 PR 07-MAY-1998; 98US-0084637P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 13-MAY-1998; 98US-0085323P.
 PR 13-MAY-1998; 98US-0085338P.
 PR 13-MAY-1998; 98US-0085339P.
 PR 15-MAY-1998; 98US-0085573P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085689P.
 PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 15-MAY-1998; 98US-0085704P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086332P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 30-JUL-1998; 98US-0087208P.
 PR 11-SEP-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 XX WPI; 1999-551358/46.
 DR P-FSDB; AA41723.
 DR
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.
 XX
 PS Claim 2; Fig 90; 530pp; English.
 PS
 XX The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as sources
 CC of probes, primers, for chromosome mapping, and for generation of
 CC antisense sequences. They can also be used to create transgenic animals.
 CC The proteins can be used to treat a variety of diseases and disorders,
 CC depending on their function. Diseases that may be treated include blood
 CC coagulation disorders, cancers and cellular adhesion disorders. They may
 CC also be used to raise antibodies. AA33891 to AA34338, and AA41685 to
 CC AA41774 represent polynucleotide and polypeptide sequence given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 2456 BP; 528 A; 719 C; 666 G; 543 T; 0 U; 0 Other;
 Query March 51.1%; Score 1013; DB 2; Length 2456;
 Best Local Similarity 78.2%; Pred. No. 6.6e-254;
 Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;
 QY 224 GGTGCTTGACACCAAGAGCGCTCAAGTGGTCCACCAATATGGAACCTTCGAAGGAAA 283
 Dd 388 GGTGCTTGACACCAAGAGCGCTCAAGTGGTCCACCAATATGGAACCTTCGAAGGAAA 447
 QY 284 CAGATGATGTGGGGAAGACACCGATCCAAAGTCTTTTAGGAGTCCCTTCTCCAGACT 343
 Dd 448 CAGATGATGTGGGGAAGACACCGATCCAAAGTCTTTTAGGAGTCCCTTCTCCAGACT 507
 QY 344 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTCGAAAGGAATCAGA 403

[illegible]

D _b	1531	-----ATATCACAAGGACGAGTACCACTTTGGTGGAG	1566
Q _y	1364	GAGTACCTGGACAATGTCAATGACGATGACTGGAAGATGCTACGAACCGTATGATGGAC	1423
D _b	1567	GAGTACCTGGACAATGTCAATGACGATGACTGGAAGATGCTACGAACCGTATGATGGAC	1626
Q _y	1424	ATAGTTCAAGATGCCACTTTTCGTGTATGCCACACTGCAGACTGCTACTACCAACCAGAT	1483
D _b	1627	ATAGTTCAAGATGCCACTTTTCGTGTATGCCACACTGCAGACTGCTACTACCAACCAG--	1683
Q _y	1484	GCGGGCTCCCTGTCCTACCTGTATGAATTTGAGCACCACGCTCGTGGATAATCGTCAAA	1543
D _b	1684	-----	1803
Q _y	1544	CCCCGCACTGATGGGGCAGACCATGGGGATGAGATGTACTTCCTTTTGGGGGCCCTTC	1603
D _b	1684	-----	1683
Q _y	1604	GCCACAGGCTTTCCATGGGTAGGAGAAAGGCACCTTAGCCTCCAGATGATGAATACTGG	1663
D _b	1684	-----	1683
Q _y	1664	GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGCCACCGCTAC	1723
D _b	1684	-----GAAACCCCAATGATGGGHAATCTGCCCTGCTGCCACCGCTAC	1724
Q _y	1724	AACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCAAGAGTGGGCGATGAAGCTCAAG	1783
D _b	1725	AACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCAAGAGTGGGCGATGAAGCTCAAG	1784
Q _y	1784	GAGAAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAAGCAGAGG	1843
D _b	1785	GAGAAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAAGCAGAGG	1844
Q _y	1844	CAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGGCCCCACCATCCAGG	1903
D _b	1845	CAATTCTAAGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGGCCCCACCATCCAGG	1904
Q _y	1904	CCCTGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTTACCACA	1952
D _b	1905	CCCTGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTTACCACA	1953

RESULT, T. 5

AAC78509

AAC78505
 ID AAC78509 standard; cDNA; 2456 BP.

AAC78509:

DT 08-FEB-2001 (first entry)

XX
DE Human PRQ873 (INO440) nucleotide sequence SEQ ID NO: 253.

xx Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
kw expressed sequence tag; detection; cancer; ss.

XX Homo sapiens.

AA WO200053756-A2.

14-SEP-2000

XX
PF 18-FEB-2000: 2000WO-US004341.XX
PR 08-MAR-1999: 99WQ-US005028.

PK 08-MAR-1999; 33WC-03003023
PR 12-MAR-1999; 99US-01239572

FR 12-MAR-1999; 99US-0126773P;
PR 29-MAR-1999; 99US-0126773P;

PR 21-APR-1999; 99US-0130232P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.

PR 26-JUL-1999; 99US-0145698P.

PR 29-OCT-1999; 99US-0162506P.

Db 1684 ----- 1683
 QY 1664 GCCAATTGTCCTCCGACAGAAACCCCAATGATGAGGAAATCTGCTGTGGCCAGCTAC 1723
 Db 1684 -----GAAACCCCAATGATGAGGAAATCTGCTGTGGCCAGCTAC 1724
 QY 1724 AACAGGATGAAAGTACCTGACGCTGGATTTTACCACAGAGTGGGCATGAAGTCTCAAG 1783
 Db 1725 AACAGGATGAAAGTACCTGACGCTGGATTTTACCACAGAGTGGGCATGAAGTCTCAAG 1784
 QY 1784 GAGAAGAAGTGGCTTTTGGATGATCTGTACCACTCTCAAGAGCTGAGAAGCAGAGG 1843
 Db 1785 GAGAAGAAGTGGCTTTTGGATGATCTGTACCACTCTCAAGAGCTGAGAAGCAGAGG 1844
 QY 1844 CAATTCTAAGGGTGGCTATGACAGAAAGGAGCCAAAGAGGGTTTGCCCCACCATCCAGG 1903
 Db 1845 CAATTCTAAGGGTGGCTATGACAGAAAGGAGCCAAAGAGGGTTTGCCCCACCATCCAGG 1904
 QY 1904 CCTGGGGAGACTAGCCATGACATACCTGGGACAAAGAGTTCTTACCCA 1952
 Db 1905 CCTGGGGAGACTAGCCATGACATACCTGGGACAAAGAGTTCTTACCCA 1953

RESULT 6

AAS45953
 ID AAS45953 standard; cDNA; 2456 BP.

XX AC AAS45953;
 XX DT 18-DEC-2001 (first entry)
 XX DE Human DNA encoding PRO polypeptide sequence #29.

XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
 KW PCR primer.

XX OS Homo sapiens.

XX PN WO200168848-A2.

XX PD 20-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006520.

XX PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 06-MAR-2000; 2000US-0186568P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 30-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US0068439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.

PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 26-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-602746/68.
 XX P-PSDB; AAU29052.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.

XX Claim 2; Fig 57; 77app; English.

CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumour in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders

XX SQ Sequence 2456 BP; 528 A; 719 C; 666 G; 543 T; 0 U; 0 Other;

Query Match 51.1%; Score 1013; DB 4; Length 2456;
 Best Local Similarity 78.2%; Pred. No. 6.6e-254;
 Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;
 QY 224 GGTGCTTGACACACAGAGGCTCAAGTGTACCAAAATATGAAACCTTCAGAGAAA 283
 Db 388 GGTGCTTGACACACAGAGGCTCAAGTGTACCAAAATATGAAACCTTCAGAGAAA 447
 QY 284 CAGATGATGTGGGAAGACACCCATCCAGTCTTTTAGGAGTCCCTTCTCCAGACCT 343
 Db 448 CAGATGATGTGGGAAGACACCCATCCAGTCTTTTAGGAGTCCCTTCTCCAGACCT 507
 QY 344 CCTTAGGTATCTCAGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 403
 Db 508 CCTTAGGTATCTCAGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 567
 QY 404 GATGCTACCACTACCGCCCTG----- 425
 Db 568 GATGCTACCACTACCGCCCTGGAATGGAGTCTCCTCTGTGCCAGGCTGGAGTGCAGTG 627
 QY 426 ----- 425
 Db 628 GCACGATCTGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGCCTCAG 687
 QY 426 -----GGTGCCTCAGAGAGTCTCTGGGGCCAGCTGGCCCTCGATG 463

[illegible]

Db	1684	-----	168
Qy	1544	CCCCGCACTGATGGGCAGACCATGGGGATGAGATGTACTTCCTCTTTGGGGCCCCCTTC	1603
Db	1684	-----	1683
Qy	1604	CCACAGGCCTTTCCATGGGTAAGGAGAAGGCACCTTAGCCTCCAGATGATGAATACTGG	1663
Db	1684	-----	1683
Qy	1664	GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC	1723
Db	1684	-----GAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC	1724
Qy	1724	AACAGGATGAAAGTACCTGCGAGCTGGATTTTACCAAGAGTGGGCATGAAGCTCAAG	1783
Db	1725	AACAAGGATGAAAGTACCTGCGAGCTGGATTTTACCAAGAGTGGGCATGAAGCTCAAG	1784
Qy	1784	GAGAAGAAGATGCTTTTTCGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG	1843
Db	1785	GAGAAGAAGATGCTTTTTCGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGG	1844
Qy	1844	CAATTCTAAGGTTGGCTATCCAGGAAGGAGCCAAAAGAGGGTTTGGCCCCCACCATCCAGG	1903
Db	1845	CAATTCTAAGGTTGGCTATCCAGGAAGGAGCCAAAAGAGGGTTTGGCCCCCACCATCCAGG	1904
Qy	1904	CCCTGGGAGACTAGCCATGCGACATACCTGGGACACAGAGTTCCTACCCCA	1952
Db	1905	CCCTGGGAGACTAGCCATGCGACATACCTGGGACACAGAGTTCCTACCCCA	1953

RESULT 7
 ABX78556
 ID: ABX78556.standard; cDNA; 2456 BP.
 XX AC ABX78556;
 XX DT
 XX DT 15-APR-2003 (first entry)
 XX DE Human PRO polynucleotide #29.
 XX DE
 KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
 KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
 KW antibody-dependent enzyme mediated prodrug therapy.
 XX XX
 OS Homo sapiens.
 XX XX
 XX US2003027272-A1.
 XX XX
 XX PD 06-FEB-2003.
 XX XX
 XX XX 21-JUN-2002; 2002US-00176492.
 XX XX
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082589P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083532P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
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PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088325P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089511P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
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RESULT 8
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KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
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Best Local Similarity			78.2%; Pred. No. 5.6e-254;
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QY	344	CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA	403
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QY	1064	ATGAGATTCTTCAACTGAACTTCCAGAGACACCGGAGAGATTTATGCTGCATGAGC	1123
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QY	1124	CCTGTGGTGGATGCTGTGATCCAGATACCCCTTTGGTGGCTCTGACCCAGGGGAG	1183
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QY	1184	GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACCACTGGAAATTCATTTGCTCTTGCCT	1243
DB	1468	GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACCACTGGAAATTCATTTGCTCTTGCCT	1527
QY	1244	TATATCATGAAGTTTCCCGCTAAACCGGACGCGATGAGAAAGGAAACCATCACTAAGATG	1303
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QY	1364	GAGTACCTGGACAAATGATGAGCATGCTGGAGATGCTACGAAACCGTATGATGAC	1423
DB	1567	GAGTACCTGGACAAATGATGAGCATGCTGGAGATGCTACGAAACCGTATGATGAC	1626

QY	1424	ATAGTTCAGATGCCACTTTTCGTGTATGCCACACTGCAGACTGCTCACTACCAACGAGAT	1483	PR	13-NOV-1997;	97US-0065311P
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QY	1484	GCCGGCCTCCCTGCTCTACCTGTATGATTTTGACACCAACGCTCGTGGATATTCGTCAA	1543	PR	12-DEC-1997;	97US-0069425P
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DT 05-AUG-2003 (first entry)
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.
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PD 06-FEB-2003.
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XX 05-AUG-2003 (first entry)

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XX Homo sapiens.

XX CS

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Db	1684	-----	1683

Qy	1604	GCCACAGGCTTTCCATGGGTAAGGAGAGGCACCTTAGCCTCCAGATGATGAAATACTGG	1663
Db	1684	-----	1683
Qy	1664	GCCAACTTTGCCCCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGCCACGCTAC	1723
Db	1684	-----GAAACCCCAATGATGGGAATCTGCCCTGCTGCCACGCTAC	1724
Qy	1724	AACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAAGCTCAAG	1783
Db	1725	AACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAAGCTCAAG	1784
Qy	1784	GAGAAGAAGATGGCTTTTGGATGAGTCTGTACCAAGTCTCAAAGACCTGAGAAGCAGAGG	1843
Db	1785	GAGAAGAAGATGGCTTTTGGATGAGTCTGTACCAAGTCTCAAAGACCTGAGAAGCAGAGG	1844
Qy	1844	CAATCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGTTTGCCCCCACCATCCAGG	1903
Db	1845	CAATCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGTTTGCCCCCACCATCCAGG	1904
Qy	1904	CCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTTACCCA	1952
Db	1905	CCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTTACCCA	1953

Search completed: August 11, 2004, 11:27:00
Job time : 833.458 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 10:48:23 ; Search time 143.88 Seconds
(without alignments)
7648.493 Million cell updates/sec

Title: US-10-001-227-1
Perfect score: 1983
Sequence: 1 ccttagcaaatcgccga.....gtttaaactgcaggactag 1983

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NR:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	424	21.4	1701	3	US-09-264-737-3
2	272.8	13.8	1746	4	US-10-023-515-3
3	272.8	13.8	2158	4	US-10-023-515-1
4	148.2	7.5	1845	1	US-07-732-962A-1
5	148.2	7.5	1845	5	PCT-US92-06106-1
6	148.2	7.5	2256	2	US-08-318-826A-5
7	148.2	7.5	2256	2	US-08-370-156-1
8	148.2	7.5	2256	3	US-08-814-095-1
9	148.2	7.5	3016	2	US-08-318-826A-7
10	148.2	7.5	3016	2	US-08-370-156-5
11	148.2	7.5	3016	3	US-08-814-095-5
12	148.2	7.5	3096	2	US-08-318-826A-6
13	148.2	7.5	3096	2	US-08-370-156-3
14	148.2	7.5	3096	3	US-08-814-095-3
15	137.2	6.9	35060	3	US-08-814-095-7
16	124.4	6.3	2184	1	US-08-445-050-8
17	124.4	6.3	2184	1	US-08-204-691-8
18	124.4	6.3	2428	1	US-08-445-050-1
19	124.4	6.3	2428	1	US-08-204-691-1
20	124.4	6.3	2428	3	US-09-355-295B-2
21	124.4	6.3	2487	3	US-08-370-223-12
22	124.4	6.3	3018	1	US-08-347-718B-3
23	124.4	6.3	3018	1	US-08-482-262-3
24	124.4	6.3	3018	6	S200183-1
25	122.8	6.2	2344	4	US-09-347-878-31
26	117	5.9	1905	4	US-09-347-878-33
27	117	5.9	1907	1	US-08-462-884A-2

ALIGNMENTS

RESULT 1

US-09-264-737-3
; Sequence 3, Application US/09264737A
; Patent No. 6107549
; GENERAL INFORMATION:
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Ruff, Thomas G.
; TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
; TITLE OF INVENTION: Expression of Esterase Enzymes
; FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
; CURRENT APPLICATION NUMBER: US/09/264,737A
; CURRENT FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: 60/077,377
; EARLIER FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Rabbit
US-09-264-737-3

Query Match	21.4%;	Score 424;	DB 3;	Length 1701;
Best Local Similarity	57.0%;	Pred. No. 4e-106;		
Matches	860;	Conservative	0;	Mismatches 635; Indels 15; Gaps 4;
QY	305	CCCATCCAGTCTTTTAGGAGTCCCTCTCCAGACCTCTCTAGGTATCCTCAGGTTT	364	
Db	139	CCCGTGGCGTCTTCTGGAGTCCCTTCGCAAGCCCTCTTGGATCCCTGAGTTT	198	
QY	365	GCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGAGATGCTACCACTACCGGCT	424	
Db	199	GCACCACACACGCTGCAGATCATGTGAGCCACGTGAAGACACACCTCTACCTCC	258	
QY	425	GGGTGCTCCAGAGTC-----CTGGGCGAGTGGCTCGATGATGTCAGACCGGGA	481	
Db	259	ATGTGCTCCAGGAGCGCAGTATCAGGGCATATGCTTCGGAGCTTTTACACCAAGAAA	318	
QY	482	CGGTACAGTGGTGGCTTCAGCGAGGACTCTGTGTACCTGACCTGTACCGCGCGG	541	
Db	319	GAGACATCCCTTTAAGTTTCTGAAGCTGCTTACCTGATATTTACACCTGCT	378	
QY	542	CGCGCGCGCGGATCCCGAGTGGTGTGTTCCCGGAGGCGGCTTATC	601	
Db	379	GACCTGACAAAGAGAGGAGGCTGCGGTGATGGTGGATCCATGGAGGTGCTGATG	438	
QY	602	GTGGGGGCTGCTTCTTCGTACGAGGCTCTGTACTTGGCGCGCGGAGAAAGTGGTGTG	661	
Db	439	GTGGGTGAGATCAACCTATGATGCTGCTTCTTGTCCCATGAGAACGTGGTGTG	498	

Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 13, Appli
Sequence 21, Appli
Sequence 31, Appli
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Sequence 19, Appli
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Sequence 5, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 1, Appli

662 GTGTTTCTGCAGCAGGCTCGGATCTTTCGGCTTCTTGAGCAGGAGCAGCAGCCAGCG 721
 499 GTGACCATTCAGTACCGCTGGGATCTGGGATCTTCAGCAGGAGATGAGCAGCAGC 558
 722 CGCGGAACTGGGGCTCTGGAACAGATGCGGCTCTGCGCTGGGTGCGAGGAACATC 781
 559 CGAGGAACTGGGGTCACTTGCACAGGTGGTGGCTGGGTGGTCCAGGACAAATTT 618
 782 GCAGCTTCGGGGAGACCCAGGAAATGTGACCTGTTCGGCAGTCGCGGGGCCATG 841
 619 GCCAACTTTGAGGGGACCCAGGCTCTGTGACCATCTTTGGAGAGTCAGCAGGAGTCAA 678
 842 AGCATCTCAGGACTGATGATCTACCCCTAGCCTCGGGTCTTTCATCGGGCAATTTCC 901
 679 AGTGCTCTATCTTATATATCCCTGACCAAGAAATCTTCCATCGAGCAATTTCC 738
 902 CAGAGTGCACCGCGTTATTCAGACTTTTCACTACTAGTAACCCACTGAAAGTGGCAAG 961
 739 GAGAGTGGCGTGGCCCTCTTTCAGTCTCTTCAGGAAGAACACCAAGTCTTTGGCTGAG 798
 962 AAGGTTGCCACCTGGCTGGATGCAACACAAACAGCAGACAGATCTCTGGTAAACTGCGTG 1021
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 1022 AGGCACTATCAGGACCAAGGTGATGGTGTGTCACCAAGATGAGATTCCTTCCAACTG 1081
 859 CGCCAGAGACAGAGGAGAACTCATGGAGTGACATTTGAAATGAAATTTATGGCTCTA 918
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 919 GATCTAGTTGCGACCCCAAGAGAACACCGCTTCTGACCACTGTGATGTGAGGGTG 978
 1142 GTGATCCAGATGACCTTTGGTGTCTCTGACCCAGGAGGAGTTTCACTGTGCGCTAC 1201
 979 CTGCTGCAAAAGCACCTGCAGAGATCTGCGAGAGAAATACAAATGCTGCGCCTAC 1038
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 1099 CCACTCTCTGAAGCAAACTGGACCAAGAGACAGTACAGAACTCTTGTGGAGTCCCTAC 1158
 1319 ACCGTGTGATATCAACAGGACAGGTACCACTTGTGTTGAGAGTACCTGGCAAT 1378
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 1379 GTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGACATAGTTCAGAGATGC 1438
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 1439 ACTTTCGTATGCCACACTGCACTGCTCTACTACACCGAGATGCCGGCCTTCCCTGTG 1498
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 1556 GGGGACACCATGGGATGAGTATCTTCTCTTTGGGGGCCCTTCCGCCACAGCCCTT 1615
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 1453 GCCACAGAGAGAGATCAAACTGAGCAGATGGTATGAATATCTGCGCCAACTTTGCT 1512
 1676 CGCACAGGAACCCCAATGATGGAATCTGCCCTGCTGCCCAAGCTTACAAAGAGATGAA 1735
 1513 AGGAATGGGAATCCCAATGAGGAAGGGCTTCTCTCAATGGCCAGCATATGACTACAAGGA 1572
 1736 AAGTACTGCTGATGATTTTACCAAGAGTGGCATGAGCTCAAGAGGAAGATG 1795

Db 1573 GGTACCTGCAGATGGAGCCACCCAGGAGCCCAAGAACTGAAAGACAGGAAGTG 1632
 QY 1796 GCTTTTGGGA 1805
 Db 1633 GCTTTCTGGA 1642
 RESULT 2
 US-10-023-515-3
 ; Sequence 3, Application US/10023515
 ; Patent No. 6654091
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Roy A. J.
 ; APPLICANT: Silos-Santiago, Inmaculada
 ; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
 ; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
 ; FILE REFERENCE: 10448-122001
 ; CURRENT APPLICATION NUMBER: US/10/023,515
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: 60/256,369
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 60/279,508
 ; PRIOR FILING DATE: 2001-03-28
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1746
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-023-515-3
 Query Match 13.8%; Score 272.8; DB 4; Length 1746;
 Best Local Similarity 53.0%; Pred. No. 9.9e-65;
 Matches 812; Conservative 0; Mismatches 627; Indels 93; Gaps 7;
 QY 305 CCCATCCNAGTCTTTTAGGAGTCCCTTCTCCAGACTCTCTAGTATCTCTCAGGTTT 364
 Db 175 CTTGTGAACGTTTCTCTGGAGTCCCTTTGCTGCTCCCGCTGGATCCCTCGGATTT 234
 QY 365 GCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGAGATGCTACCACTACCCGCCCT 424
 Db 235 ACBAACCGGACCTGTCATGCCCTGGGATAAATTGGAGAGCCACTCTTACCTAAT 294
 QY 425 GGTGCTGAGGAGTCTCTGGGCGGAGTGGCTCTGATGTACGTACAGCAGCGGGAACGG 484
 Db 295 TTGTGCTCCAGAACTCAGAGTG---GCTGCTCTTAGATCAACACATGCTCAAGGTGAT 351
 QY 485 TACAAGTGGCTCGCTTTCAGCGGAGTCTGTACCTGAACGTGTACGCGCGCGCGCGC 544
 Db 352 TACCGGAATTCGAGTGTGAGAGACTGCTCTACTGAACTATCTATGCGCTGCCAC 411
 QY 545 GCGCCCGGGGATCCCGAGCTGCCAGTATGGTCTGTTCCCGGAGCGCTTTCATGCTG 604
 Db 412 GCCGATACAGGCTCCAAGCTCCCGCTCTTGGTGTGTTCCAGAGGTGCTTCAAGACT 471
 QY 605 GGCCTGCTTCTTCTGACGAGGCTGACTTGGCGCGCGCGCGAGAAAGTGTGCTGGTG 664
 Db 472 GGCTACGCTTCCATCTTTGATGGTGGCTCGCTTATGAGGACGTGCTGGTTGTG 531
 QY 665 TTCTGAGCAGCAGGCTCGGCATCTTTCGGCTTCTTCCAGCAGGACGACACGCCAGCGCGC 724
 Db 532 GTCTCCAGTACCGGCTAGGAATATTTGGTTTCTTCCACATGGGATCAGATGCTCCG 591
 QY 725 GGGAACTGGGGGCTGCTGGACCAAGTGGCGCTCTGGCTGGTGGAGAGACATCGCA 784
 Db 592 GGGAACTGGGGCTTCAAGGACCAAGTGGCTGCTCTGCTGGTCCAGAGGACATCGAG 651
 QY 785 GCCTTCGGGGGAGACCCAGGAAATGTGACCTGTTCCGGCAGTCCGGCGGGGCCATGAGC 844
 Db 652 TTCTTCGTTGGGACCCAGCTCTGTGACCATCTTTGGGAGTCCCGGGAGGACCAAGT 711
 QY 845 ATCTCAGGACTGATGATGTACCCCTAGCTCGGCTCTTCCATCGGGCCATTTCCAG 904

Db 712 GTTCTTCTAGTCTTATCTAGTCTCCATGGCCAAAGGCTTATCCACAAAGCCATCATGGAG 771
Qy 905 AGTGGCACCGGTATTCAGACTTTTCATCACTAGTAACCCACTGA-----AGTGGCC 958
Db 772 AGTGGGTGGCCATCATCCCTTACCTGGAGGCCATGATATAGAGAGAGTAGGACCTG 931
Qy 959 AAGAAGGTTGCCACCTGGGTGGATGCAACCAACAGCAGCAGACAGATCTCTGTGTAAACTGC 1018
Db 832 CAGGTGTTGCACATTTCTGTGTAAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGC 891
Qy 1019 CTGAGGSCATATCAGGACCAAGGTGATCGGTGTCTCAACAAGATGAGATCTCTCCAA 1078
Db 892 CTGAGGACAAACCCCTCAAGGAGCTGCTGACCCCTAGCCAGAAACAA----- 940
Qy 1079 CTGAATCTCCAGAGAGACCGGAAGAGATATCTGTTCCATGAGCCCTGTGTGGATGGT 1138
Db 941 -----AGTCTTTCATCGAGTGGTGTGATGT 966
Qy 1139 GTGTGATCCAGATGACCTTTGGTGTCTCTGACCCAGGGAAGTTTCATCTGTGCC 1198
Db 967 GCCTTCTTCTTATGAGCTCTAGATCTATTGCTCTCAGAAAGCATTTAAAGCAATCCT 1026
Qy 1199 TACCTTCTAGTGTCAACAACCTGGAATTCAAATGGCTCTTGCTTATATCATGAAGTTC 1258
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Qy 1379 GTCAATGAGCATGATCTGAAGATGCTACGAACCGTATGATGACATAGTTCGAAGTGC 1438
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Qy 1439 ACTTTCGTGTATGCCACACTGCAGACTGCTCACTACCAACGAGATGCCGCTCCCTGTC 1498
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Db 1309 TACTTCTATGATTTTGGCACCGGCCCTCAGTGCTTTGAAGACAGAACCGGCTTTTGTG 1368
Qy 1557 -GGGACACCATGGGATGATGATGATCTTCTCTTTGGGGCCCTTCGCCACAGGCTT 1615
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Db 1429 ATTGTTATGTCGAAGGACCCAGAGGAGAGAGTGTACTGAGCCGGAAGATGATGAAA 1488
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Db 1609 CTCAAAGAACCGGGTGGATTTTGGACCAG 1640

RESULT 3
US-10-023-515-1
; Sequence 1, Application US/10023515
; Patent No. 6664091
; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)....(1838)
US-10-023-515-1

Query Match 13.8%; Score 272.8; DB 4; Length 2158;
Best Local Similarity 53.0%; Pred. No. 1.1e-64;
Matches 812; Conservative 0; Mismatches 627; Indels 93; Gaps 7;

Qy 305 CCCATCCCAAGTCTTTTAGGAGTCCCTTCTCCAGACCTCCTCTAGGTATCTCTCAGTTT 364
Db 270 CTTGTGAAGTGTCTCTCGAGTCCCTTGTGTCTCCCGCTGGGATCCTCTGCGATT 329
Qy 365 GCACCTCCAGAACCCCGAGCCCTGGAAGAAATCAGAGATGCTTACCTTACCTTACCGGCT 424
Db 330 ACGAACCCGAGCTGCTGCTGCTGGGATAAATTTGCGAAGAGCCACCTCTTACCCCTAAT 389
Qy 425 GGTGCTCTCAGAGTCTCTGGGCGGAGCTGGCTGCTGATGCTAGCTCAGCACGGGAAACGG 484
Db 390 TTGTGCTCTCAGAACTCAGAGTG-----GCTGCTCTTAGATCAACATGCTCAAGTGTGAT 446
Qy 485 TACAAGTGTCTCGCTTTCAGCAGGAGTCTGTGTACCTGAACGTGTACGCGCGCGCGCG 544
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Db 507 GCGGATACAGGCTCCAAAGCTCCCGTCTTGTGTGTTTCCCGAGGAGTCTTCAAGACT 566
Qy 605 GCGCTGTCTTCTGTACAGGAGTCTGACTTTGGCGCGCGCGGAGAAAGTGTGTGCTGTG 664
Db 567 GGTCTAGCTCTCATCTTTGATGGTCCGCCCTGGCTGCTATGAGGACGTGCTGTGTG 626
Qy 665 TTTCTGACACAGGCTCGCATCTTCGGCTTCTTGTAGCAGGAGCAGCAGCCACCGCGCG 724
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Qy 725 GGAAGTGGGGCTGTGGACCAAGTGGGCTCTGCGCTGGTGCAGGAAACATCGCA 784
Db 687 GGAAGTGGGGCTTCAAGACCAAGTGGTGTCTGTCTGCTGGGTCCAGAGAACATCGAG 746
Qy 785 GCCTTCGGGGAGACCCAGAAATGTGACCTTTCGGCCAGTCTGGCGGGGCGCATGAGC 844
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Qy 845 ATCTCAGGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
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Qy 905 AGTGGCACCGCGTTATTTCAGACTTTTTCATCACTAGTAAACCCACTGA-----AAGTGGCC 958
Db 867 AGTGGGTGGCCATCATCTTACCTTGGAGGCCCATGATTATGAGAGAGTGGAGACCTG 926
Qy 959 AAGAAGTTGCCACCTGGCTGATGCAACCAACAGCAGCAGACAGATCTCTGTGTAACATGC 1018
Db 927 CAGGTGTTGCACATTTCTGTGTAAACAATGCTCAGACTCTGAGGCCCTCTGTGAGGTGC 986

QY 1019 CTGAGGGCACTATCAGGAGCAAGGTGATGGTGTGCTCCAAACAAGATGAGATTCCTCCAA 1078
| | | | |
Db 987 CTGAGGACAAACCCCTCCAGGAGCTGCTGACCTCAGCCAGCAAAACAA----- 1035
QY 1079 CTGAACCTCCAGAGAGACCGGAGAGATTATCTGCTCCATGAGCCCTGCTGGTGGTGT 1138
| | | | |
Db 1036 -----AGCTTTTCATCGAGTGTGATGGT 1061
QY 1139 GTGTGTATCCAGATGACCTTTTGTGCTCCTGACCCAGGGAAGTTTATCTGTGCC 1198
| | | | |
Db 1062 GCTTTCTTTCTAATGAGCTCTAGATCTATTGCTCAGAAAGCATTTAAAGCAATTCCT 1121
QY 1199 TACCTTCTAGGTCAACAAGCTGGAATTCATTTGGCTCTTGGCTTATATCATGAGTTC 1258
| | | | |
Db 1122 TCCATCTCGGAGTCAATAACACGAGTGTGGCTTCTGCTGCTATGAAGAGGCTCCT 1181
QY 1259 CCGCTAAACCGGAGGCGATGAGAAAGAAACCAATCACTAAGATGCTCTGGAGTACCGGC 1318
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Db 1182 GAGATCCTCAGTGGCTCCACAAGTCCCTTGCCTCCATCTGAT-----ACAA 1229
QY 1319 ACCCTGTTGAATATACCAAGAGCAGGTACCACTTGTGTGGAGGAGTACCTGGACAAT 1378
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Db 1230 AACATCTCGACATCCCGCTCAGTATTGACCTTGTGCTAATGAATATCTTCCA--- 1285
QY 1379 GTCAATGAGCATGACTGGAAGATGCTAGAAACCGTATGATGACATAGTTCAGATGCC 1438
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Db 1286 --TGACAGCACTCCCTGACTGAATCCGAGACAGTCTTCTGACTTGTGGAGATGT 1343
QY 1439 ACTTTGTGTATGCCACACTGCTCAGACTGCTACCTACCAAGAGATGCCGCTCCTGTGC 1498
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Db 1344 TTCTTTGTGTGCTCCCTGACCTGATCAGACCTCGATATCAGAGATGCTGTGACCTGTC 1403
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Db 1404 TACTTCTATGATTTGCGACCGGCTCAGTCTTTGAAAGACAGAACCGGCTTTTGTG 1463
QY 1557 -GGGACAGCATGGGATGAGATGATCTTCTTTTGGGGGCCCCCTTGCACAGGCCCC 1615
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Db 1464 AAAGCCAGCAGCTGATGAATCCGCTTTGTGTGCTGGTGGTCTTCTGAGGGGGGAC 1523
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| | | | |
Db 1524 ATTGTTATGTTGAGAGAGCCAGGAGGAGAGATTTCTGAGCCGGAAGATGATGAA 1583
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Db 1584 TACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGCTCTGTGCGCA 1643
QY 1718 CGCTACAAACAGGATGAAAGTACCTGACCTGATTTTACCAAGAGTGGGATGAAG 1777
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Db 1644 GCTTATAATCTGACTGAGAGTACCTCCAGCTGGACTTGAACATGAGCCTCGACACAGA 1703
QY 1778 CTCAAGGAGAGAGATGCTTTTGGATCAG 1809
| | | | |
Db 1704 CTCAAGAACCGGGTGGATTTTGACCCAG 1735

RESULT 4

US-07-732-962A-1
; Sequence 1, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fisher, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732.962A
FILING DATE: 19910722
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1842
US-07-732-962A-1

Query Match 7.5%; Score 148.2; DB 1; Length 1845;
Best Local Similarity 48.3%; Pred. No. 1.3e-30;

Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

QY 305 CCCATCCAAGTCTTTTAGGAGTCCCTTTCTCCAGACCTCTCTAGTATCTCTCAGGTTT 364
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Db 175 CTTGTCTCTGCTTTCTCTGGGATCCCTTTCTCGGAGCCACCCATGGACCCCTCGCTTT 234
QY 365 GCACCTCCAGAACCCCGGAGCCCTGGAAAGAAATCAGAGATGTCACCTACCTCCCT 424
| | | | |
Db 235 CTGCCACCGAGCCCAAGACGCTTGTGAGGGGTGTAGACGCTACAACTTCCAGT 294
QY 425 GGTGCTCTGAGAGTCTCTGGGCGCAGCTGGCCCTGATGTACGTACGACGCGGGAACGG 484
| | | | |
Db 295 GTCTGTACCAATATGT---GGACACCTATACCCAGGTTTTCAGGCGCAGAGATGTG 351
QY 485 TACAAGTGGCTGCTTCAGCGAGAGCTGTCTACCTGACGTGACGCGCGCGCGCGC 544
| | | | |
Db 352 AACCCCACTGTAGCTGAGCGAGAGTCTGCTGTACCTAACGTTGAGACACATACCCC 411
QY 545 CGCCCGGGGATCCCAAGTCTCCAGTGTGTTTCCCGGAGCGCTTTCATCGTG 604
| | | | |
Db 412 CGGCC---TACATCCCCACCCCTGTCTCTGCTGGATCTATGGGGTGGCTTCTACAGT 468
QY 605 GGCCTGCTCTT-----CGTAGAGGCTCTGACTTGGCCCGCCCGGAGAGTGTG 658
| | | | |
Db 469 GGGGCTCTCTCTTGAGAGCTGTACGATGGGCGCTTCTTGTGTACAGGCGGAGAGCTGTG 528
QY 659 CTGGTGTCTTCTGACACAGGCTCGGCATCTTCTGGCTTCTCTGAGACGCGACGAGCC-- 716
| | | | |
Db 529 CTGGTGTCTTCTGAGTCTACCGGGTGGGAGCTTTGGCTTCTCTGGCCCTGCGGGGAGCGA 588
QY 717 -ACCGCGGGGAACCTGGGCTCTGAGACAGATGCGGCTCTGCTGGTGTGAGGAG 775
| | | | |
Db 589 GAGCCCGGGCAATGTGGTCTCTCTGGATCAGAGCTGGCCCTGAGTGGGTGCGAGGAG 648
QY 776 AACATCGAGCTTCGGGGGAGACCCAGGAAATGTGACCTGTTTCGCCAGTCCGGGGG 835
| | | | |
Db 649 AACGTGGAGCTTCGGGGGTGACCCACATCAGTGACGCTGTTTGGGAGAGCGCGGA 708
QY 836 GCCATGAGCATCTCAGGACTGATGTACCCCTAGCTCGGGTCTCTTCCATCGGGCC 895
| | | | |
Db 709 GCGCCTCGTGGGAGTGCACCTGCTCTCCCGCCCGGAGCGGGGCTGTTCACAGGGCC 768

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QY 896 ATTTCCAGAGTGG-----CACGGCGTTATTTCAGACTTTTTCATCTACTAGTACCCACTG 949
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Db 829 CGCAGGCCCAAGAGTGGCCCACTTGTGGGTGTCTTCCAGCGGCACTGGTGGGAAT 888
QY 1010 GTAACGTGCTGAGGGCACTATCAGGACCAAGTGTGATGCTGTGTCACCAAGATGAGA 1069
Db 889 GACACAGAGTGGTAGCTGCTTCGGACACAGCAGCGCAGGTCTCTGGTGAA----- 941
QY 1070 TTCTCCCACTGAATCTTCAGAGAGACCCCGAAGAGATTATCTGGTCCATGAGCCCTGTG 1129
Db 942 --CACGAATGGCAGCTGCTCCCTCAAGAAAGGTCTTCCGGTCTCTCTCGTGGCTGTG 999
QY 1130 GTGATGGTGTGGTATCCAGATGACCTTTGGTGTCTCTGACCCAGGGAGAGTTTCA 1189
Db 1000 GTAGTGGAGATCTTCCCTCAGTGACACCCAGAGGCCCTCATCAACGGGAGAGACTTCCAC 1059
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QY 1550 ACTGATGGGCGAGACCATGGGATGAGATGATCTCTCTTTGGGGCCCTT---CGCC 1606
Db 1417 TGGATGGGGTGGCCCAACCGCTACGAGATCGAGTTCATCTTGGGATCCCCCTGGACCCC 1476
QY 1607 ACAGGCTTTCCATGGGTAAAGGAGAGGCACTTAGCCCTCCAGATGATGAATACTGGGC 1666
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QY 1667 AACTTTGCCCGCACAGGAACCCCAATGA 1695
Db 1537 AACTTTGCCCGCACAGGGGATCCCAATGA 1565
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PCT-US92-06106-1
; Sequence 1, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
; PCT-US92-06106-1
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Query Match 7.5%; Score 148.2; DB 5; Length 1845;
Best Local Similarity 48.3%; Pred No. 1.3e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

QY 305 CCATTCGAAGTCTTTTATAGGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCTAGGTTT 364
Db 175 CCGTCTCTGCTTTCTGGGATCCCTTTGGGAGCCACCCATGGGACCCGCTGCTTT 234
QY 365 GCACCTCCAGAGACCCCGGAGCCCTGGAAGAAATCAGAGATGCTACACCTACCCGCT 424
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QY 717 -ACGCGCGCGGAACCTGGGGGCTGTGACACAGATGGCGGTCTGCGGTGCGTGCAGAG 775
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QY 776 AACATCGCAGCTTCGGGGAGACCCAGGAATGTGACCTGTTCGGCCAGTTCGCGGGGG 835
Db 649 AACGTGGCAGCTTCGGGGGTGACCCGACATCAGTGAAGCTGTTTGGGGAGAGCCGGA 708
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Db 709 GCGGCTCGGTGGGATGCACTGTCTGCTCCCGCCAGCCGCGGGCTGTTCACAGGGCC 768
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 QY 1130 GTGATGTTGGTGTATCCAGATGACCTTTGGTGTCTCTGACCCAGGGAAGTTTCA 1189
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 Db 1537 AACTTTCCCGCAGGAGATCCCAATGA 1565

RESULT 6

US-08-318-826A-5
 ; Sequence 5, Application US/0831826A
 ; Patent No. 5891725
 ; GENERAL INFORMATION:
 ; APPLICANT: Sored, Hermona
 ; APPLICANT: Zukut, Haim
 ; APPLICANT: Eckstein, Fritz
 ; TITLE OF INVENTION: Synthetic Antisense
 ; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
 ; CITY: Farmington Hills

STATE: Michigan
 COUNTRY: US
 ZIP: 48334
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/318,826A
 APPLICATION NUMBER: US/08/318,826A
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30,955
 REFERENCE/DOCKET NUMBER: 2391.00001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (248) 539-5050
 TELEFAX: (248) 539-5055
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2256 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,
 OTHER INFORMATION: 3, 4 and 5"
 US-08-318-826A-5

Query Match 7.5%; Score 148.2; DB 2; Length 2256;
 Best Local Similarity 48.3%; Pred. No. 1.4e-30;
 Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;
 QY 305 CCCATCCAAAGCTTTTAGGAGTCCCTTCTCCAGACTCTCTCTAGTATCTCTCAGTTT 364
 Db 334 CTTGTCTCTGTTCTCTGGCATCCCTTTGCGGAGCACCCTATGGACCCCTCGCTTT 393
 QY 365 GCACCTCCAGAACCCCGAGCCTGGAAAGGATCAGAGATGCTACCACTACCCGCT 424
 Db- 394 CTGCCACCGAGCCCAAGCAGCTTGGTCAGGGTGGTAGACGTCAACCTTCCAGAT 453
 QY 425 GGTGCTCTGAGGAGTCTCTGGGCGCAGCTGGCTCGATGTACGTACAGCAGCGGGAACGG 484
 Db 454 GTCTGTACCAATATGT---GGACACCTATACCAGTTTGTAGGCGCACCGAGATGG 510
 QY 485 TACAAAGTGGCTGGCTTTCAGCGAGGACTGTCTGTACCTGAACGTGTAGCGCGCGCGC 544
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 Db 571 CGGCC---TACATCCCCACCCCTGCTCTGTGGATCTATGGGGTGGCTTCTACAGT 627
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 Db 628 GGGGCTCTCTCTGGACGTGTAGCATGGCGCTTCTTGTGTACAGGCGCGAGGACTGTG 687
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Db 808 AACGTGGCAGCCTTCGGGGGTGACCCGACATCAGTGACGCTGTTTGGGAGAGCGCGGA 867
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QY 1430 CAAGATGCCATTTCTGTGTATGCCACACTGACAGACTGCTCACTACCACCGAGATGCCGC 1489
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QY 1550 ACTGATGGGCGAGACCATGGGATGAGATGATCTCTTCTTGGGGCCCTT- - - - -CGCC 1606
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QY 1607 ACAGGCTTTCCATGGGTAGGAGAGGCACTTAGCCTCCAGATGATGAATACTGGGC 1666
Db 1636 TCTCGAAATACACGGCAGAGGAAATCTTCCAGGAGCACTGATGCGATATCTGGGC 1695
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RESULT 7

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; US-08-370-156-1
; Sequence 1, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES

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; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-1

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Query Match 7.5%; Score 148.2; DB 2; Length 2256;
Best Local Similarity 48.3%; Pred. No. 1.4e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

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QY 305 CCATCCCAAGTCTTTTAGGAGTCCCTTCTCCAGACCTCTCTAGTATCTCTCAGGTTT 364
Db 334 CTTGCTCTGCTTTCTTGGGATCCCTTTGGGAGCCACCCATGGGACCCGCTGCTT 393
QY 365 GCACCTTCAGAAACCCCGAGCCCTGGAAGAATCAGAGATGCTACACCTACCCGCT 424
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Db 454 GTCTGCTACCAATATGT- - - - -GGACACCTATACCCAGGTTTGGGGCACCGAGATG 510
QY 485 TACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACTTGAACGTTACGCGCGCGCGC 544
Db 511 AACCCCAACCGTAGCTGAGCGAGGACTGCTGTACTCTCAACGCTGTGGACACCATACCCC 570
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QY 605 GCGCGTGTCTTCTT- - - - -CGTACGAGGGCTCTGACTTGGCGCGCCGCGAGAAAGTGTG 658
Db 628 GGGGCTCTCTCTCGACGCTGTACGATGCGCGCTTCTTGGTACAGCGCGAGAGGACTGTG 687
QY 659 CTGCTGTTTTCAGCAGCAGGCTCGGCTCTTGGCTTCTTGGCTTCTTGGCTTCTTGGCTT 716
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Db 808 AACGTGGGAGCCTTCGGGGGTGACCCGACATCAGTACGCTGTTTGGGGAGAGCGCGGA 867
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RESULT 8
US-08-814-095-1
; Sequence 1, Application US/0814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Screeg, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES

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; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLSCULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "ACHE gene comprising exons
; DESCRIPTION: 2, 3, 4 and 6"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-814-095-1

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Query Match 7.5%; Score 148.2; DB 3; Length 2256;
Best Local Similarity 48.3%; Pred. No. 1.4e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

QY 305 CCCATCCAAAGTCTTTTAGGAGTCCCTTCACAGACCTCTCTAGGTATCTCTCAGGTTT 364
Db 334 CTGTCTCTGTTTCTCTGGCATCCCTTTGCGGAGCCACCCATGGACCCCGTCTGTTT 393
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QY 776 AACATCGAGCCTTCGGGGGAGACCCAGGAAATGTGACCTGTTCGGCCAGTCGCGCGGG 835

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Db 808 AACGTGACAGCTTCGGGGTGACCCGACATCAGTACGCTGTTTGGGGAGAGCGCGGA 867
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Db 868 GCGCCCTCGGTGGGCATGCACCTGCTGCTCCCGCCGACCGCGGCGCTGTTCCACAGGGCC 927
Qy 896 ATTTCGCCAGAGTG- - - - -CACCAGGTTATTACAGATTTTCATCATCTACTATACCACTG 949
Db 928 GTGCTGCAGAGCGGTGCCCCCATATGACCTGGGCCACGGTGGGCATGGGAGGCGCCGT 987
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Db 1219 GGCCTGACAGTGTGGTGGTGTGGTGAAGATGAGGCTCGTATTTCTGTTTACGGG 1278
Qy 1250 ATGAAGTTCGGCTTAACCGGCGAGCGATGAGAAAGAAACCATCATAGATGCTCTGG 1309
Db 1279 GCCCAGGCTTCAGAAAGACACAGAGTCTCTCATCAGCGGCGGAGTTCCTGGCGGG 1338
Qy 1310 AGTACCGCACCTGTTGAATATACCAAGAGCAGGTACCACTTGTGTTGAGGAGTAC 1369
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Qy 1430 CAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCACTACCAAGATGCGGC 1489
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RESULT 9

US-08-318-826A-7
; Sequence 7, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense

; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
; OTHER INFORMATION: /note= "Splice Variant: Exons 1, 2,
; OTHER INFORMATION: 3, 4, 5 and 6"
US-08-318-826A-7

Query Match 7.5%; Score 148.2; DB 2; Length 3016;
Best Local Similarity 48.3%; Pred. No. 1.6e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;
Qy 305 CCCATCCCAAGTCTTTTAGGAGTCCCTTCTCCAGACCTCCTTAGGTATCCTCAGGTTT 364
Db 334 CTGTCTCTGCTTCTCTGGGATCCCTTTGGGAGCCACCCATGGGACCCGTCGCTT 393
Qy 365 GCACCTCCAGAACCCCGAGCCCTGGAAAGAAATCAGAGATGCTACCACTACCCGCT 424
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Db 454 GTCTGCTACCAATATGT- - - - -GGACACCTATACCCAGGTTTGGGGCACCAGATGTGG 510
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Qy 605 GCGGCTGCTTCTT- - - - -CGTACGAGGCTCTGTACTTTGGCGCCCGCGAGAAAGTGGT 658
Db 628 GGGGCTCTCTCTTGGACGTGTACCATGGCCGCTTCTTGGTACAGCGCGAGAGGACTGTG 687
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Db	748	GAGGCCCGGCAATGTGGGTCTCTCTGATCAGAGGCTGGCCCTGCAGTGGTGCAGGAG	807
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Db	1219	GGCCTGCAGGTGTGTGGTGTGGTGAAGGATGAGGGCTCGTATTTCTTGGTTTACGGG	1278
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Qy	1490	CTCCCTGTCTACCTGTATGAATTTGACACACAGCTCGTGGAAATAATCGTCAAAACCCCGC	1549
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Qy	1550	ACTGATGGGGAGACCAATGGGATGAGATGTACTTCTCTTTGGGGGCCCTT---CGCC	1606
Db	1576	TGATGGGGGTGCCCAACGGCTACGAGATCGAGTTCACTTTGGGATCCCTCTGGACCCC	1635
Qy	1607	ACAGGCCCTTTCCATTTGGTAAAGAGAGGCACTTAGCCTCCAGATGATGAATAACTGGCC	1666
Db	1636	TCTCGAACTACACGGCAGAGGAGAAATCTTCGCCACGCACTGATCGATCTGGCC	1695
Qy	1667	AACTTTCCCGCACAGGAAACCCCAATGA	1695
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US-08-370-156-5
Sequence 5, Application US/08370156
Patent No. 5932780
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: US
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370.156
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-307 (Mulford)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 689-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3016 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 160..2010
US-08-370-156-5

Query Match	7.5%;	Score 148.2;	DB 2;	Length 3016;
Best Local Similarity	48.3%;	Pred. No. 1.6e-30;		
Matches 680;	Conservative	0;	Mismatches 693;	Indels 36; Gaps 8
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Db	394	CTGCACCGGAGC	CCCAAGACGCTTGTTCAGGGGTGGTAGAGCTACA	ACCTTCCAGAGT 453
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Db	628	GGGGCTCTCTCT	TGGACGTGTACGATGGCCGCTTCTTGGTAC	AGCCGAGAGGAGTGTG 687
Qy	659	CTGTGTGTTCTG	CAGCAAGGCTCGGCATCTTCGGCTTCTCTGAGCAGCGACGAC	AGCC- -- 716

Db	688	CTGGTGTCCATGAACACCGGGTGGAGCCTTTGGCTTCTTGCCCTTCGCGGAGCCGA	747
Qy	717	-ACGCGCGCGGAACCTGGGGCTCTGTGGAACAGATGGCGCTCTGGCGTGGTGCAGGAG	775
Db	748	GAGGCCCGGGAATGTGGGTCTCTGGATCAGAGGCTGCCCCCTGCAGTGGTGCAGGAG	807
Qy	776	AACATGCGACCTTTCGGGGAGAGCCAGGAAATGTGACCTGTTCGGCCAGTCGGCGGG	835
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Db	928	GTGCTGCAGAGCGGTGCCCCCAATGAGCCCTGGGCCACCGTGGGCATGGAGAGGCCGT	987
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Db	1048	GACACAGAGCTGTAGCTCCCTTCGGACACGACGCGAGGTCCTGTGTGA- ----	1100
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Db	1101	--CCAGNATGGCAGCTGTGCTGCCTCAAGAAGCGCTTTCCGGTTCTCTCTGTCCTGTG	1158
Qy	1130	GTGGATGGTGTGTGATCCAGATGACCTTTGGTGTCTCTGACCCAGGGAAGTTTCA	1189
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Db	1219	GGCCTGCAAGTGTGGTGGTGTGGTGAAGATGAGGCTTCGTATTCTTGTTTACGGG	1278
Qy	1250	ATGAAGTTCCTCGTTAAACCGCGAGGCGATGAGAAAGGAACCATCACTAAGATGCTCTGG	1309
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Db	1636	TCTCGAACTACAGGCAGAGAGAAATCTTCCGCCAGCGACTGATGCCGATCTGGGCC	1695
Qy	1667	AACTTTGGCCGCA CAGGAAACCCCAATGA	1695
Db	1696	AACTTTGGCCGCA CAGGGGATCCCAATGA	1724

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US-08-014-095-5
; Sequence 5, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Scorg, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/POCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Alternatively spliced AChE
; DESCRIPTION: comprising exons 2, 3, 4, 5 and 6"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
US-08-814-095-5

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Query Match 7.5%; Score 148.2; DB 3; Length 3016;
Best Local Similarity 48.3%; Pred. No. 1.6e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

QY	305	CCCATCAAGTCTTTTTAGGAGTCCCCTTCTCCAGACCTCTCTAGGTATCCTCAGGTTT	364
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Db	511	AACCCCAACCTGTGAGCTAGCGAGGACGTGCTGTACTCAACGTGTGGACACCATACCC	570
QY	545	CGCGCCGGGGATCCCCAGCTGCCAGTGAATGTCTGGTTCCGGGAGGCGCTTCACTGTG	604
Db	571	CGGCC---TACATCCCCACCCCTGTCTCTCTCTGGATCTATGGGGGTGGGTTCTACAGT	627

QY 605 GGGCTGCTTCTT-----CGTACAGGGCTCTGACTTGGCCGCCCGGAGAAAGTGGTG 658
Db 628 GGGGCTCTCTCTTGGAGCGTGTACGATGGCGCTTCTTGGTACAGGCGCGAGAGACTGTG 687
QY 659 CTGTGTTTCTGACGACAGGCTCGGCATCTTCGGCTTCTGAGACGGACGACAGCC-- 716
Db 688 CTGTGTCCATGACTACCGGCTGGAGCCCTTGGCTTCTGCGCTCGCGGGAGCCGA 747
QY 717 -ACGCGCGCGGAACACTGGGGCTCTCTGACACAGATGGCGCTCTGCGCTGGTGCAGGAG 775
Db 748 GAGGCGCGCGGAATGTGGTCTCTCTGATCAGAGGCTGGCCCTCGAGTGGGTGCAGGAG 807
QY 776 AACATCGCAGCTTCGGGGGAGACCCAGGAATGTGACCTGTTCGCCCAAGTCCGGGGG 835
Db 808 AACGTGGCAGCTTCGGGGGTGACCCACATCAGTACGCTGTTTGGGGAGAGCGGGGA 867
QY 836 GCCATGAGCATCTCAGGACATGATGTCAACCTAGCCTCGGTCTCTTCCATCGGGCC 895
Db 868 GCGGCTCGGTGGGCATGCACTCTGTCCCGGCCAGCGGGCGCTGTTCCACAGGGCC 927
QY 896 ATTTCCGAGTGG-----CACCGCTTATTCAGACTTTTCATCTACTAGTAAACCACTG 949
Db 928 GTGTGACAGCGGTGCCCCCAATGGACCTTGGGCCACGGTGGGCTATGGAGAGGCCGT 987
QY 950 AAAGTGGCCAAAGAGTTGCCACCTGGCTGGATGCAACACACACACACACAGCATCCTG 1009
Db 988 CGCAGGGCCAGCAGCTGGCCACCTTGTGGCTGTCTCCAGCGCGCACTGTGTGGAAT 1047
QY 1010 GTAACCTGCTGAGGGCACTATCAGGACCAAGGTGATCGTGTCTTCCACAGATGAGA 1069
Db 1048 GACACAGAGCTGTAGCTGCTTTCGACACAGCCAGCGCAGCTCTGTGTGAA----- 1100
QY 1070 TCTCTCAACTGAATCTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTG 1129
Db 1101 --CCACGATGGCAGCTGTCTCCACAGAAAGCGTCTTCGGTTCCTCTGTCCTGTG 1158
QY 1130 GTGATGGTGTGTATCCAGATGACCTTTGTGTCTGACCCAGGGAAGGTTCAT 1189
Db 1159 GTAGATGAGACTTCTCAGTGACACCCAGAGCCCTCATCAACGCGGAGACTTCCAC 1218
QY 1190 TCTGTGCTTACCTTCTAGTGTCAACACCTGAATTCATTTGGCTCTTGCCTTATATC 1249
Db 1219 GCGCTGACAGT 1278
QY 1250 ATGAAGTTCGCGTAAACCGCGAGCGATGAGAAAGAAACCATCACTAAGATGCTCTG 1309
Db 1279 GCGCCAGGCTTCAGAAAGACACAGCTCTCTCATCAGCGCGCGAGTTCCTGCGCGG 1338
QY 1310 AGTACCGCACCTGTGTATATACCAAGAGACAGTACCATCTGTGTGGAGGATAC 1369
Db 1339 GTGCGGTGCGGGTTCCTCCAGTAAAGTGAACCTGGACCGAGGCTGTGGTCTGCTATAC 1398
QY 1370 CTGACAAATGTCAATGAGCATGATGAGATGCTACGAAACCGTATGATGAGCATAGTT 1429
Db 1399 ACAGCTGGCTGATCCGAGGACCGCGCAGCTGTAGGAGAGCCCTGTAGCGATGTGGTG 1458
QY 1430 CAAGATGCCACTTTCGCTGTATGCCACTGCACTGCACTGCTCACTACACCGAGATGCCGG 1489
Db 1459 GCGACACCAATGTGTGTGCGCGGTGGCCAGCTGTGGGCGATGTGCTGCCAGGT 1518
QY 1490 CTCCTCTCTACCTGTATGAATTTGACACACAGGCTGTGGAATAATCTGCAAAACCCCG 1549
Db 1519 GCGCGGTCTAGCGCTTGT 1575
QY 1550 ACTGATGGGAGACCACTAGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606
Db 1576 TGGATGGGGTGGCCACGCTACGAGATCGAGTTCATCTTTGGGATCCCTTGGACCCC 1635
QY 1607 ACAGGCTTTTCCATGGGTGAGGAGAGGCACTTATAGCTCCAGATGATGAATACTGGGC 1666
Db 1636 TCTGAAACTACAGGCGAGAGGAGAAATCTTCCCGCAGGCACTGATGCTACTTGGGC 1695
QY 1667 AACTTTCCCGCAGAGAAACCCCAATGA 1695

Db 1696 AACTTTGCCGACAGGGGATCCCAATGA 1724

RESULT 12

US-08-318-826A-6

; Sequence 6, Application US/08318826A

; Patent No. 5891725

; GENERAL INFORMATION:

; APPLICANT: Sored, Hermona

; APPLICANT: Zakut, Haim

; APPLICANT: Eckstein, Fritz

; TITLE OF INVENTION: Synthetic Antisense

; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions

; TITLE OF INVENTION: Containing them

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kohn & Associates

; STREET: 30500 No. 5991725thwestern Hwy., Suite 410

; CITY: Farmington Hills

; STATE: Michigan

; COUNTRY: US

; ZIP: 48334

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/318,826A

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Kohn, Kenneth I.

; REGISTRATION NUMBER: 30,955

; REFERENCE/DOCKET NUMBER: 2391.00001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (248) 539-5050

; TELEFAX: (248) 539-5055

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3096 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cdna to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 160..1959

; OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,

; OTHER INFORMATION: 3, 4, 5 and the translated portion of Intron 4 (readthrough)"

US-08-318-826A-6

Query Match

Best Local Similarity 7.5%; Score 148.2; DB 2; Length 3096;

Matches 680; Conservative 48.3%; Pred. No. 1.6e-30;

Mismatches 693; Indels 36; Gaps 8;

QY 305 CCCATCCAAAGCTTTTGGAGTCCCTCTCCAGAGCTCTCTAGGTATCTCAGGTTT 364

Db 334 CTTGCTCTGCTTCTTGGGATCCCTTTGGGAGCCACCCATGGAGCCCGCTGCTTT 393

QY 365 GCACCTCCAGAACCCCGAGCCCTGGAAAGGAATCAGATGATACCACTACCGCCCT 424

Db 394 CTGCCACCGGAGCCCAAGAGCCCTTGGTCAAGGCTGTAGACGCTACCACTTCCAGAGT 453

QY 425 GGGTGCCTGACAGGAGTCTGGGGCCAGCTGGCTCTGATGTACGTACACCGCGGAACGG 484

Db 454 GTCTGTACCAATATGT---GGACACCTATACCCAGTTTGGAGGCAACCGAGATGTGG 510

485 TACAAGTGGCTGGCTTACGAGGAGTGTCTGTACCTGAACGTGTACCGCGCGGCGGC 544
511 AACCCCAACGCTGAGCTGAGCGAGGACTGCTGTACCTCAACGTGTGACACATACCCC 570
545 GCACCGGGGATCCCGAGCTGCCAGTGGCTGTCTCCCGGAGCGCTTCTACGTG 604
571 CGGCC---TACATCCCGACCCCTGCTGCTGTGATCTATGAGGCTGTCTACAGT 627
605 GGGCGCTGCTTCTT-----CGTACGAGGGGTCTGACTTGGCCCGCCGAGAAAGTGTG 658
628 GGGCGCTGCTTCTTGGAGGTGTACGATGGCGCTTCTTGGTACAGCGCGAGAGGACTGTG 687
659 CTGGTGTCTGACGACAGGCTGGCATCTTCGGCTTCTGAGTCTGAGCAGCGACGACGACG-- 716
688 CTGGTGTCTGATGAATACCGGTGGGAGCTTGTGCTTCTGCGCTTCTGCGGAGCGCA 747
717 -AGCGCGCGGGAACCTGGGGGCTGCTGGACAGATGGCGGCTCTGCGTGGTGGTGCAGGAG 775
748 GAGGCCCGGGCAATGTGGGTCTCTTGGATCAGAGGCTGGCCCTGCAGTGGTGCAGGAG 807
776 AACATGCGACCTTGGGGGAGACCCAGGAAATGTGACCTCTGTTCGGCAGTGGCGGGG 835
808 AACGTGCGACCTTGGGGGTGACCCGACATCAGTACGCTGTGTGGGAGAGCGCGGGA 867
836 GCCATGAGCATCAGGACTGATGTACCCCTAGCTCGGGTCTTTCATCGGGC 895
868 GCGCGCTGGTGGCATGACCTGTCTGCTCCCGCCAGCGGGGCTGTTCACAGGCGC 927
896 ATTTCCAGAGTGG-----CACCGGTATTACAGACTTTTTCATCACTAGTAACCACTG 949
928 GTGCTGACAGCGGTGCCCCCAATGGACCTTGGGCCACCGTGGGCTGGGAGAGCGCGT 987
950 AAGTGGCCAGAGGTTGCCACCTGGCTGGATGCAACACACAGCACACAGATCCTTG 1009
988 CGCAGGCGCCAGCAGCTGGGCCACCTTGTGGGTGCTCTCAGCGGCACTGTGGGAAT 1047
1010 GTAACTGCTGAGGGCACTATCAGGACCAAGGTGATGGTGTGTCCAAACAAGATGAGA 1069
1048 GACACAGAGCTGTAGCTGCTCTCGGACACAGCACGCGCAGGTCTCTGGTGA-- 1100
1070 TTCCTCAACTGAATCTTCAGAGAGACCCGGAAGATTAATCTGGTCCATGAGCCCTGTG 1129
1101 --CACGAATGGCAGCTGCTGCTCAAGAAAGGCTCTTCCGGTCTCTTCTGTGCTGTG 1158
1130 GTGATGGTGTGGTATCCAGATGACCTTGTGTCTCTGACCCAGGGGAAGGTTTCA 1189
1159 GTAGTGGAGACTTCTCAGTGACACCCAGAGCCCTCATCAACGCGGAGACTTCCAC 1218
1190 TCTGTGCTTACTTCTAGGTGTCAACACCTGGAATTCATTTGGCTCTTGCCTTATATC 1249
1219 GGCCTGCAAGTGTGGTGGTGTGGTGAAGATGAGGGCTCGTATTTCTGGTTACGGG 1278
1250 ATGAAGTTCGGCTAAACCGGCGAGCGATGAGAAAGAAACCATCACTAAGATGCTCTGG 1309
1279 GCGCAGGCTTCAGCAAGAACAGAGTCTCTCATACCGCGGCGGAGTTCTTGGCGGG 1338
1310 AGTACCGCACCTTGTGAATATACCAAGAGAGGATACACTTGTGTGGTGGAGGATAC 1369
1339 GTGCGGTGGGGTTCGCCAGCTAAGTACCTGCGCAGCGAGGCTGTGGTCTGCAATTAC 1398
1370 CTGACATGTCAATGACATGACTGGAAGTGTAGCAACCGATGATGATGGACATAGTT 1429
1399 ACAGACTGGCTGCATCCCGAGGACCGGACGCTGAGGAGGCGCTGAGGATGTGGT 1458
1430 CAAGATGCGACTTTCGTGTATGCCACACTGACAGACTGCTCACTACCAACCGAGATGCGGC 1489
1459 GCGACCAACAATGTCGTGCCCCGTGGCCAGCTGGCTGGCGACTGGGTGCCAGGCT 1518
1490 CTCCTGTCTACGTGTGAATTTGAGCACACAGCTGTGGAATAATGTCATAACCCCGC 1549
1519 GCGCGGTCTAGGCTTACGCTTTTGAACACCGCTG---TTCACGCTCTCTGCGCCCTG 1575
1550 ACTGATGGGGCAGACCATGGGGATGAGATGTACTTCTTCTTGGGGGCGCCCTT---CGCC 1606

1576 TGGATGGGGTGGCCCCACGGCTACGAGATCAGTTCACTTTGGGATCCCCCTGGACCCC 1635
1607 ACAGCGCTTTCCATGGGTAAAGGAGAGGCACTTAGCTTCCAGATGATGAATACTGGGCC 1666
1636 TCTCGAAACTACACGGCAGAGGAGAAAATCTTCGCCAGCGACTGATCGGATACTGGGCC 1695
1667 AACTTTCGCCGACAGGAAACCCCAATGA 1695
1696 AACTTTGCCGACAGGGGATCCCAATGA 1724

RESULT 13
US-08-370-156-3
; Sequence 3, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370.156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..1959
; US-08-370-156-3

Query Match 7.5%; Score 148.2; DB 2; Length 3096;
Best Local Similarity 48.3%; Pred. No. 1.6e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

305 CCATCCAGTCTTTTAGGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCAGGTTT 364
334 CTGTCTGTCTTCTCTGGGATCCCTTTGGGAGCCACCCATGGACCCCGTCTT 393
365 GCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGAGATGCTACACCTACCGCT 424
394 CTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGCGCTACACCTTCCAGAGT 453
425 GGGTGCCTCAGAGGTCCTGGGGCCAGCTGGCTGATGTCAGTACGACCGGGAACGG 484
454 GTCTGTACCAATATGT---GGACACCTTATACCCAGGTTTGGAGGACCCGAGATGTGG 510

Qy	485	TACAAGTGGTGCGCTTCAGCGAGCACTGTCTGTACTCTGAACAGTGTTACGCGCGCGCGCGC	544
Db	511	AACCCCAACCGTGAGCTGAGCGAGGACTGCGCTGTACCTCAACGTGTGGACACCATACCC	570
Qy	545	GCSCCCGGGGATCCCCAGCTGCCAGTGCCTGTTCCGGGAGGCGCTTCATCGT	604
Db	571	CGGCC--TACATCCCCACCCTGTCTCTGTCTGGATCTATGGGGTGGCTTCTACAGT	627
Qy	605	GGCGCTGCTCTTT-----CGTACAGGGCTCTGACTTGGCCCGCCCGAGAGAAAGTG	658
Db	628	GGGGCTCTCTCTTGGACGTGTACGATGGCGCTTCTTGGTACAGGCCGAGAGGACTGTG	687
Qy	659	CTGGTCTTTCTGCGACACAGGCTGGCATCTTCGGCTTCTTGAGCAGGACGACACAGCC--	716
Db	688	CTGGTTCATGAATACCGGGTGGAGCCCTTGGCTTCTGGCCCTCGCGGGAGCCGA	747
Qy	717	AGCGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGCTCTGGCTGGGTGACGAG	775
Db	748	GAGGCCCGGGCAATGTGGTCTCTGGATCAGAGGCTGGCCCTGCAGTGGGTGCGAGAG	807
Qy	776	AACATCGGAGCCTTCGGGGGAGACCCAGGAAATGTGACCTGTTCGGCCAGTTCGCGGG	835
Db	808	AACGTGGACGCTTCGGGGGTGACCCGACATCAGTACGCTGTTTGGGAGAGCGCGGA	867
Qy	836	GCCATGAGCATCTCAGGACTGATGATGTCACCCTAGCCTCGGGTCTCTTCATCGGGC	895
Db	868	GCCGCTCGTGGGCATGCACTCTCTCCCGCCAGCGGGGCTGTTCACAGGCC	927
Qy	896	ATTTCACAGTGG-----CACCGGTTATTAGACTTTTCATCTACTAGTAACCACTG	949
Db	928	GTGTGTCAGAGCGGTGCCCCAAATGGACCTTGGGCCACGGTGGGATGGAGAGCCCGT	987
Qy	950	AAAGTGGCCAAAGGTTGCCACCTGGCTGGATGCAACACAAACAGCACACAGATCTGT	1009
Db	988	CGAGGGCCACGACCTGGCCCACTTGTGGGTGTCTCTCAGGGGCACTGGTGGGAAT	1047
Qy	1010	GTAAACTGCCTGAGGGCACTATCAGGACCAAGGTGATGCTGTGTCTCAACAAGATGAGA	1069
Db	1048	GACACAGAGCTGGTAGCTGCTTTCGACACGACCGAGCGAGCTCCTGTGTAA-----	1100
Qy	1070	TTCCTTCAACTGAATTCACAGAGACCGGAGAGATTAATCTGGTCCATGAGCCCTGTG	1129
Db	1101	--CCAGTAATGGCAGTCTGCCTCAAGAAAGCGTCTTCGGTCTCTCTGTGGTCTGTG	1158
Qy	1130	GTGGATGTGTGGTGATCCAGATGACCTTGGTGCTCTGACCCAGGGGAAGGTTTCA	1189
Db	1159	GTAGATGGAGACTTCTCAGTGACACCCACAGAGCCCTCATCAACGCGGAGACTTCCAC	1218
Qy	1190	TCGTGGCCTTACCTTAGGTGTCAACACTGGAAATTCAAATTGGGCTCTTGCTTTATATC	1249
Db	1219	GGCCTGCAAGTGTGTGGTGGTGTGGTAGAGGATGAGGGCTCGTATTTTCTGTTTACGG	1278
Qy	1250	ATGAAGTTCCCGCTAAACCGCGAGCGGATGAGAAAGAAACCATCACTAAGATGCTCTGG	1309
Db	1279	GCCCCAGGCTTCACGAAGACACAGAGTCTCTCATCAGCCGGGCCAGTTCTTGCCCGGG	1338
Qy	1310	AGTACCCGACCCCTGTTGAATATACCAAGAGACAGGTACCACTTGTGGTGGAGAGTAC	1369
Db	1339	GTGCGGGTTCGGGGTTTCCCAAGTGAAGTGACCTGGCAGCGAGGCTGTGTCTGCAATTAC	1398
Qy	1370	CTGGACAATGTCAATGAGCATGACTGGAAGATGCTACTAGAAACCGTATGATGGACATGTT	1429
Db	1399	ACAGACTGGCTGCATCCGAGGACCCGGCAGCCTGAGGAGGGCCCTGAGCGATGTGGTG	1458
Qy	1430	CAAGATGCCATTTGGTGTATGCCACACTGACAGACTGTCTACTACACCGAGATGCCGGC	1489
Db	1459	GGCGACCACAATGCTGTGCCCCGTGGCCAGCTGGCTGGCGACTGGCTGCCAGGGT	1518
Qy	1490	CTCCCTGTCTACCTGTATGAATTGAGCACCAAGCTGTGGAAATTAATGCTCAAAACCCCGC	1549
Db	1519	GCCCGGTCTACGCCTACGTCTTTGAACACCGTGC---TTCACAGCTCTCTGTGCCCTGT	1575
Qy	1550	ACTGATGGGCAGACCATGGGGATGAGATGTACTTCTCTTTGGGGGGCCCCCTT---GGCC	1606

Db	1576	TGATGGGGTGGCCACGGCTACGAGTCGAGTTCATCTTTGGGATCCCCCTGGACCCC	1635
Qy	1607	ACAGGCCCTTCCATGGGTAGGAGAGGCCACTTAGCTCCAGATGATGAATACTCGGGCC	1666
Db	1636	TCTCGAACTACACGGCAGAGGAGAAATCTTCCACGCGACTGATCGGACTCGGGCC	1695
Qy	1667	AACTTTCCCGCACAGGAAACCCCAATGA	1695
Db	1696	AACTTTCCCGCACAGGGATCCCAATGA	1724

RESULT 14

US-08-814-095-3
Sequence 3, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Sored, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "alternatively spliced ACHE
DESCRIPTION: comprising exons 2, 3, 4 and 5 as well as
DESCRIPTION: of Intron 4 (readthrough)"
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 160..1959
US-08-814-095-3

Query Match 7.5%; Score 148.2; DB 3; Length 3096;
Best Local Similarity 48.3%; Pred. NO. 1.6e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36;

[illegible]

Db 394 CTCCACCGAGGCCAAGCAGGCTTGGTCAAGGGTGGTAGACGCTACAACTTCCAGAGT 453
Qy 425 GGGTGGCTCAGAGAGTCTGGGCGCCAGCTGGCTCGATGTAGTACGACGCGGGAACGG 484
Db 454 GTCTGTACCAATATGT---GGACACCTTATACCCAGGTTTGGAGGCAACCGAGATGTGG 510
Qy 485 TACAAGTGGTGGCTTACGAGAGGACTGTCTGTACTGAAAGTGTACGCGCGGCGGC 544
Db 511 AACCCCAACCGTAGCTGAGCGAGGACTGCTGTACTCAAGTGTGGACACATACCC 570
Qy 545 GCGCGCGGGATCCCGAGCTGCCAGTGTGGTCTGGTTCGCGGAGGCGCTTCTATCGTG 604
Db 571 CGGCC---TACATCCCCACCTCTCTCGTCTGATCTATGGGGTGGCTTCTACAGT 627
Qy 605 GGCCTGCTCTTT---CGTACGAGGGCTTGAATTTGGCCCGCCCGAGAGAGTGTG 658
Db 628 GGGGCTCTCTCTTGGAGCTGTACGATGGCGCTTCTTGTGTACAGCCGAGAGGACTGTG 687
Qy 659 CTGGTGTCTGAGACAGCTCGCATCTCTGGCTTCTGAGTGTGAGCAGGACAGACGCC-- 716
Db 688 CTGGTGTCTGATGATACCGGTGGAGCTTTGGCTTCTGCGCTTGGCGGGAGCGCA 747
Qy 717 -ACGCGCGCGGAACTGGGGCTGTGGACAGATGGCGCTGTGGTGGTGGTGGTGGAG 775
Db 748 GAGGCCCGGCAATGTGGTCTCTGGATCAGAGGCTGGCCCTGCGTGGTGGTGGAG 807
Qy 776 AACATCGAGCTTCGGGGAGACCCAGGAATGTGACCTGTTCGCCAGTGGCGGG 835
Db 808 AAGTGGACCTTCGGGGGTGACCCGACATCATGTGACCTGTTCGGGAGAGCGCGGA 867
Qy 836 GCCATGAGCATCTCAGGACTGATGTACCCCTAGCCTCGGCTCTTCCATCGGGCC 895
Db 868 GCGGCTCGTGGGATGACCTGTCTGCTCCCGCCAGCGGGGCTGTTCACAGGGCC 927
Qy 896 ATTTCCAGAGTG---CACGGCTTATCAGACTTTTATCATCTAGTAAACCCACTG 949
Db 928 GTGCTGAGAGCGGTGCCCCCAATGAGCTGGGCCACGCTGGGCACTGGAGAGGCCGT 987
Qy 950 AAGTGCCCAAGAGTGTCCACCTGGCTGGATGCAACCAACACACACACAGATCTGTG 1009
Db 988 CGAGGGCCACGAGCTGGGCCCTTGTGGCTGTCTCCAGCGGCACTGTGGGAAT 1047
Qy 1010 GTAACCTGCTAGGGCACTATAGGACCAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 1069
Db 1048 GACACAGAGTGTGTAGCTGCTTCCGACACACAGCAGCGAGTCTCTGTGTAA----- 1100
Qy 1070 TTCTCCCACTGATCTCCAGAGAGCCCGAAGAGATTTCTGTCTCATGAGCCTGTG 1129
Db 1101 --CACGAATGGACGCTGCTCCCTCAAGAAGCGTCTTCGGTTCCTCTGCTGCTGTG 1158
Qy 1130 GTGATGTGTGTGATCCAGATGACCTTTGTGTCTGTGACCCAGGGGAAAGTTTCA 1189
Db 1159 GTAGTGGAGACTTCTCAGTGACACCCAGAGGCTCTCATCAAGCGGAGACTTCCAC 1218
Qy 1190 TCTGTGCTTACCTTCTAGTGTCAACACTGGAATTCATTTGGCTTTCCTTATATC 1249
Db 1219 GGCCTGCAAGTGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1278
Qy 1250 ATGAAGTTCGCGCTAAACCGGCGATGAGAAAGGAACCATCACTAAGATGCTCTGG 1309
Db 1279 GCGCCAGCTTCAGCAAGACACAGAGTCTCTCATCGCGGCGAGTCTCTGCGCGGG 1338
Qy 1310 AGTACCCGACCTTCTGATATACCAAGAGAGGATACACTTGTGTGTGTGTGTGTGTGT 1369
Db 1339 GTGCGGGTGGGGTTCCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1398
Qy 1370 CTGGCAATGTCAATGAGCATGATGGAAGTGTACGAAACCGTATGATGAGATAGTT 1429
Db 1399 ACAGACTGGCTGATCCCGAGAGCCCGCAAGCTGTGAGGAGGCGCTGAGCGATGTGTG 1458
Qy 1430 CAAGATGCCACTTCTGTATGCCACACTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1489
Db 1459 GSCGACCAATGT 1518

Qy 1490 CTCCTGTCTACCTGTATGAATTTGAGCAGCAGCTGTGGAATAATCGTCAAAACCCGC 1549
Db 1519 GCCCGGTCTACGCTACGCTACGCTTTTGAACACCGTGC---TTCCAGCTCTCTGTGGCCCTG 1575
Qy 1550 ACTGATGGGCGACACCATGGGATGAGATGCTTCTTTGGGGGCGCCCT---CGCC 1606
Db 1576 TGGATGGGGTGGCCCGCTACGATCGAGTTCATCTTTGGATCCCGCTGGACCC 1635
Qy 1607 ACAGGCTTTCCATGGTGAAGGAGGACCTTAGCCTCCAGATGATGAATACTGGGCC 1666
Db 1636 TCTCGAACTACAGCGGAGGAGAAATTTGCCCGACGACTGATGCGATCTGGGCC 1695
Qy 1667 AACTTTGCCCGCAGGAAACCCCAATGA 1695
Db 1696 AACTTTGCCCGCAGGAGTCCCAATGA 1724

RESULT 15
US-08-814-095-7
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Sored, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183Western Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHE
; DESCRIPTION: promotor, ACHE gene and ARS gene"
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
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; NAME/KEY: promotor
; LOCATION: 4089..22464
; OTHER INFORMATION: /function= "ACHE Promotor"
; OTHER INFORMATION: /standard_name= "ACHE Promotor"
; FEATURE:

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/ OTHER INFORMATION: /function= "non-translated"
/ OTHER INFORMATION: /gene= "ACHE"
/ OTHER INFORMATION: /number= 1
/ FEATURE:
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/ IDENTIFICATION METHOD: experimental
/ OTHER INFORMATION: /function= "(translation start:
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/ FEATURE:
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Query Match 6.98; Score 137.2; DB 3; Length 35060;

Best Local Similarity 56.0%; Pred. No. 5.5e-27; Matches 347; Conservative 0; Mismatches 258; Indels 15; Gaps 4;

Qy 305 CCATCCAAAGTCTTTTAGGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCTCAGGTTT 364

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Qy 365 GCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGAGATGCTACCACTTACCGCCT 424

Db 24344 CTGCCACCGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGACGCTACAACTTCCAGAGT 24403

Qy 425 GGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCAGTACGTACGACGCGGGAACG 484

Db 24404 GTGTGCTACCAATATGT--GGACACCTATATACCCAGGTTTGGAGGSCACCGAGATGTGG 24460
Qy 485 TACAAGTGGTGGCTTACGAGGAGTGTCTGTACTGTAACTGTACGCGCGCGCGCGC 544
Db 24461 AACCCACCGTGAGCTAGCGAGGAGTGCCTGTACTCACTCACTGTGGACACCATACCCC 24520
Qy 545 GCGCCCGGGGATCCCAAGCTGCCAGTATGGTCTGGTTCCCGGAGGCGCCTTTCATCGTG 504
Db 24521 CGGCC--TACATCCCCCACCCTGTCTCTGTGATCTATGGGGGTGCTTCTACAGT 24577
Qy 605 GCGCTGCTTCTT-----CGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAGTGTG 658
Db 24578 GGGCCCTCCTCTTGGACGTGTACGATGGCGGCTTCTTGTACAGCCCGAGGAGTGTG 24637
Qy 659 CTGTGTGTTCTGCAGCACAGGCTCGGCATTTTCGGTTTCTGTAGCACGAGACAGACC-- 716
Db 24638 CTGTGTCCATGAATACCGGGTGGGAGCCTTTGGCTTCTCGGCCCTGCGGGAGCCGA 24697
Qy 717 -ACGCGCGCGGAACTGGGGGCTCTGGACAGATGGCGCTCTGCGTGGGTGCAGGAG 775
Db 24698 GAGCCCCCGGCAATGTGGGTCTCTGGATCAGAGGTGGCCCTGAGTGGGTGCAGGAG 24757
Qy 776 AACATCGAGCCTTCGGGGGAGACCCAGGAAATGTGACCCCTGTTCCGCCAGTCGCGGGG 835
Db 24758 AACGTGGACGCTTCGGGGTGRACCCGACATCAGTGACGCTGTTTGGGGAGAGCGCGGA 24817
Qy 836 GCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC 895
Db 24818 GCCCCTCGGTGGCATGACCTGTCTCCCGCCAGCCGGGGCCTGTTCCACAGGGCC 24877
Qy 896 ATTTCCAGAGTGCACCGC 915
Db 24878 GTGCTGCAGAGCGGTGCCCC 24897

Search completed: August 11, 2004, 18:18:24
Job time : 174.88 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 15:30:03 ; Search time 998.854 Seconds
(without alignments)
10824.678 Million cell updates/sec

Title: US-10-001-227-1

Perfect score: 1983

Sequence: 1 ccttagccaattcgccga.....gttaaacctgcaggactag 1983

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1983	100.0	1983	15	US-10-001-227-1
2	1928.6	97.3	2081	17	US-10-343-593-29
3	1752	88.4	1752	15	US-10-001-227-3
4	1459.4	73.6	2178	16	US-10-108-260A-339
5	1013	51.1	2456	9	US-09-978-295A-253
6	1013	51.1	2456	9	US-09-978-697-253
7	1013	51.1	2456	9	US-09-978-192A-253
8	1013	51.1	2456	9	US-09-999-832A-253
9	1013	51.1	2456	10	US-09-978-189-253
10	1013	51.1	2456	10	US-09-978-608A-253
11	1013	51.1	2456	10	US-09-978-585A-253
12	1013	51.1	2456	10	US-09-978-191A-253
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16 1013 51.1 2456 10 US-09-981-915A-253 Sequence 253, App

17 1013 51.1 2456 10 US-09-978-824-253 Sequence 253, App

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35 1013 51.1 2456 13 US-10-164-749A-253 Sequence 253, App

36 1013 51.1 2456 13 US-10-206-915-57 Sequence 57, Appl

37 1013 51.1 2456 13 US-10-199-670-57 Sequence 57, Appl

38 1013 51.1 2456 13 US-10-201-858-57 Sequence 57, Appl

39 1013 51.1 2456 13 US-09-999-831A-253 Sequence 253, App

40 1013 51.1 2456 13 US-10-205-890-57 Sequence 57, Appl

41 1013 51.1 2456 13 US-10-208-024-57 Sequence 57, Appl

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ALIGNMENTS

RESULT 1

US-10-001-227-1

; Sequence 1, Application US/10001227

; Publication No. US20030166900A1

; GENERAL INFORMATION:

; APPLICANT: KAPPELLER-LIBERMANN

; APPLICANT: SILOS-SANTIAGO

; TITLE OF INVENTION: METHODS OF USING 18903 TO TREAT PAIN AND

; TITLE OF INVENTION: PAIN-RELATED DISORDERS

; FILE REFERENCE: MNI-199

; CURRENT APPLICATION NUMBER: US/10/001,227

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/250929

; PRIOR FILING DATE: 2000-11-30

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1983

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (98)....(1849)

US-10-001-227-1

Query Match 100.0%; Score 1983; DB 15; Length 1983;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GATAAAAGTGTGCTCACACACTGTAGACACGGCTACCATCCACAGTTTCCCATC 120

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1921 ATGACATACCTGGGAGCAAGAGTTCACCAAGGCGGAATTCGTTTAAACCTCAGGAC 1980
1981 TAG 1983
1981 TAG 1983

RESULT 2

US-10-343-593-29
; Sequence 29, Application US/10343593
; Publication No. US20040110259A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;
; APPLICANT: BRUNS, Christopher M.; DAS, Debopriya;
; APPLICANT: DELEGENE, Angelo M.; DING, Li;
; APPLICANT: ELIOT, Vicki S.; GANDHI, Ameena R.;
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.;
; APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
; APPLICANT: LEE, Sally; LU, Dyung Aina M.;
; APPLICANT: LU, Yan; ARVIZU, Chandra S.;
; APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
; APPLICANT: SANTANWALA, Madhusudan M.; TANG, Y. Tom;
; APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael;
; APPLICANT: TRIBOULEY, Catherine M.; CHAWLA, Narinder K.;

APPLICANT: WARREN, Bridget A.; YANG, Junming;
APPLICANT: YAO, Monique G.; YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0185 USN
CURRENT APPLICATION NUMBER: US/10/343,593
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US 60/223,055
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/224,728
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/226,440
2000-08-18
PRIOR APPLICATION NUMBER: US 60/228,067
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,063
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/232,244
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: US 60/234,269
PRIOR FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PERL Program
SEQ ID NO 29
LENGTH: 2081
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7478588CB1
US-10-343-593-29

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1931; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 78 ACATGTAGACAGGCTACCATCCACAGTGTGCCATCCACAGTGTGCCATCAC 137
Db 87 ACATGTAGACAGGCTACCATCCACAGTGTGCCATCCACAGTGTGCCATCAC 146

Qy 138 TCCTGCCACAGCAGGAGCTGGTGGAGCATGAGTGGATTCTGTGCTGGAGCCTCACCC 197
Db 147 TCCTGCCACAGCAGGAGCTGGTGGAGCATGAGTGGATTCTGTGCTGGAGCCTCACCC 206

Qy 198 TCTGCCTGATGGCCGACAGCGCTTGGTGGCTTGACACACAGAGGCTCAAGTGTCA 257
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Qy 258 CCAATATGGAACCTCTCAAGGAAACAGATGATGTGGGGAAGACACACCATCCAAAGTCT 317
Db 267 CCAATATGGAACCTCTCAAGGAAACAGATGATGTGGGGAAGACACACCATCCAAAGTCT 326

Qy 318 TTTTAGAGTCCCTTCTCCAGACCTCTCTAGTATCTCTAGGTTTGCACCTCCAGAAC 377
Db 327 TTTTAGAGTCCCTTCTCCAGACCTCTCTAGGTTTGCACCTCCAGAAC 386

Qy 378 CCCCGAGCCTGGAAGGAATCAGATGCTACCACTCCCGCCTGGGTGCTGCAGG 437
Db 397 CCCCGAGCCTGGAAGGAATCAGATGCTACCACTCCCGCCTGGGTGCTGCAGG 446

Qy 438 AGTCTGGGGCAGCTGCCCTCGATGATCGTCAGCACGCGGGAACGGTCAAGTGGCTGC 497
Db 447 AGTCTGGGGCAGCTGCCCTCGATGATCGTCAGCACGCGGGAACGGTCAAGTGGCTGC 506

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Db 507 GCTTCAGGAGGACTGTCTGTACCTGACGTTACGCGCGCGCGCGCGCGCGCGGATC 566

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Db 567 CCCAGCTCCAGTGTGTCTGTTCCCGGAGGCGCTTCATCGTGGGGCTGTCTT 626

Qy 618 CGTACGAGGCTCTGACTTGGCCCGCCGAGAAAGTGGTCTGTGTCTGTCAGACACA 677
Db 627 CGTACGAGGCTCTGACTTGGCCCGCCGAGAAAGTGGTCTGTGTCTGTCAGACACA 686

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Db 687 GGCTCGGCATCTTGGCTTCTGAGCAGGACGACGACGCGCGCGGGAACCTGGGGGC 746

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Db 927 TATTGAGCTTTTTCATCTAGTAACTGAAAGTGGCCAAAGAGTTGCCACCTGG 986

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; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 09/918585
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/064249
PRIORITY FILING DATE: 1997-11-03
PRIORITY APPLICATION NUMBER: 60/065311
PRIORITY FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22

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Db 1468 GTTTCATCTGCGCCCTACCTTTCTAGGTGTCAACAACCTGGAATCAATTGGCTCTTGCCT 1527
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Qy 1304 CTCTGGAGTACCGGACCCCTTTGAAATATACCAAGAGAGGTACCACTTGTGGTGAG 1363
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Qy 1364 GAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGTCAGAAACCGTATGATGGAC 1423
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Qy 1424 ATAGTTCAGATGCCACTTTCTGTATGCCACACTGCAGACTGCTCACTACCCAGAT 1483
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Db 1684 -----1683
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Db 1684 -----GAAACCCCAATGATGGGAATCTGCCCTGCGCCACGCTAC 1724
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Db 1725 AACAGGATGAAGTACCTGACCTGGATTTACCAAGAGTGGGATGAAGCTCAAG 1784
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Qy 1904 CCCTGGGAGACTAGCCATGACATACCTGGGACAGAGTCTTACCCA 1952
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RESULT 6

US-978-697-253
; Sequence 253, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivarov, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER:	60/084637

Query Match 51.1%; Score 1013; DB 9; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.7e-292;
Matches 1445; Conservative 0; Mismatches 0; Indels 403; Gaps 3

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61	PRIOR APPLICATION NUMBER: 60/081817	61	PRIOR FILING DATE: 1998-05-15
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63	PRIOR APPLICATION NUMBER: 60/081819	63	PRIOR FILING DATE: 1998-05-15
64	PRIOR FILING DATE: 1998-04-15	64	PRIOR APPLICATION NUMBER: 60/085579
65	PRIOR APPLICATION NUMBER: 60/081952	65	PRIOR FILING DATE: 1998-05-15
66	PRIOR FILING DATE: 1998-04-15	66	PRIOR APPLICATION NUMBER: 60/085580
67	PRIOR APPLICATION NUMBER: 60/081838	67	PRIOR FILING DATE: 1998-05-15
68	PRIOR FILING DATE: 199		

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC53
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30

Qy 1604 GCCACAGGCTTTCCATGGGTAAGGAGAGGCACTTAGCCTCCAGATGATGAATACTGG 1663
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Db 1684 -----GAAACCCCAATGATGGGAATTCGCCCTGCTGGCCACGCTAC 1724
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Db 1725 AACAGGATGAAAGTAGTCTGACCTGAGTTTACCAACAAGAGTGGSCATGAAGCTCAAG 1784
Qy 1784 GAGAAGAGATGGCTTTTGGATGAGTCTTACAGTCTCAAGAGCTCAAGAGAGAGAGG 1843
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Qy 1844 CAATCTAAGGGTGGCTATCCAGGAAGGCCAAAGAGGGGTTTGGCCCAACCATCCAGG 1903
Db 1845 CAATCTAAGGGTGGCTATCCAGGAAGGCCAAAGAGGGGTTTGGCCCAACCATCCAGG 1904
Qy 1904 CCCTGGGGAGACTAGCCATGGACATACCTGGGGACAGAGTCTTACCCA 1952
Db 1905 CCCTGGGGAGACTAGCCATGGACATACCTGGGGACAGAGTCTTACCCA 1953

RESULT 9

US-09-978-189-253
; Sequence 253, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1997-11-21
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15


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QY 1064 ATGAGATTCCTCAACTGAACTTCCAGAGAGCCCGAAGAGATTATCTGGTCCATGAGC 1123
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Db 1408 CCTGTGTGATGGTGTGATGCCAGATGACCCCTTTGGTGTCTCTGACCCAGGGGAAG 1467
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Db 1785 GAGAAGAGATGGCTTTTGGATGAGTCTGTACCAAGTCTCAAGACCTGAGAAGCAGAGG 1844
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Db 1905 CCCTGGGAGACTAGCCATGACATACCTGGGAGCAGAGTCTTACCCA 1953

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RESULT 10

US-09-978-608A-253
; Sequence 253, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

```

; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PlC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 253
; LENGTH: 2456
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-608A-253

Query Match 51.1%; Score 1013; DB 10; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.7e-292;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

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QY 404 GATGCTACCACTACCCGCTG- 425
Db 568 GATGCTACCACTACCCGCTGATGAGTCTCGCTCTGCGCAGGCTGGAGTGCAGTG 627
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 QY 1124 CCTGTGTGATGGTGTGTTGATCCAGATGACCTTTGGTGTCTGACCCAGGGGAG 1183
 Db 1408 CCTGTGTGATGGTGTGTTGATCCAGATGACCTTTGGTGTCTGACCCAGGGGAG 1467
 QY 1184 GTTTCATCTGTGCTTACCTTCTAGGTGTCAACACCTGGAATTCATTTGGCTTTGGCT 1243
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RESULT 11

US-09-978-585A-253
 ; Sequence 253, Application US/09978585A
 ; Publication No. US20030049633A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C15
 ; CURRENT APPLICATION NUMBER: US/09/978,585A
 ; CURRENT FILING DATE: 2001-10-16
 ; NUMBER OF SEQ ID NOS: 624
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 253
 ; LENGTH: 2456
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-978-585A-253

Query Match 51.1%; Score 1013; DB 10; Length 2456;
 Best Local Similarity 78.2%; Pred. No. 2,7e-292;
 Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;
 QY 224 GGTGCTTGCACACCAAGAGGCTCAAGTGTGTCACCAATATGGAACCTTCGAAGAAAA 283
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344 CCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 403
508 CCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 567
404 GATGCTACCACTTACCCGCTG----- 425
568 GATGCTACCACTTACCCGCTGAGTGGAGTCTCGCTCTGTGCCAGGCTGGAGTCAGTG 627
426 ----- 425
628 GCACGATCTCGGCTCACTGCACTCCGCTCCCGGTTCAAGCGAGTCTCTGCTCAG 687
426 -----GTCCTCGAGGAGTCTGGGGCCAGCTGCCTCGATG 463
688 CCTCTAGGTCTGGGGCTACAGTGCCTGAGGAGTCTGGGGCCAGCTGCCTCGATG 747
464 TACGTGAGCAGCGGGAACGGTAAAGTGGCTGCGTTTCAAGCGAGGAGTCTGTACCTG 523
748 TACGTGAGCAGCGGGAACGGTAAAGTGGCTGCGTTTCAAGCGAGGAGTCTGTACCTG 807
524 AAGTGTGAGCG 583
808 AAGTGTGAGCG 867
584 CCGGAGGCGCGCTTCACTGCTGGCGCTGCTTCTGTCAGGAGGCTCTGACTTGGCGCC 643
868 CCGGAGGCGCGCTTCACTGCTGGCGCTGCTTCTGTCAGGAGGCTCTGACTTGGCGCC 927
644 CGGAGAAAGT 703
928 CGGAGAAAGT 987
704 ACAGGAGCAGACG 763
988 ACAGGAGCAGACG 1047
764 TGGGTGAGGAGAACATCGCAGCTTGGGGGAGACCCAGGAAATGTGACCTGTTCGCG 823
1048 TGGGTGAGGAGAACATCGCAGCTTGGGGGAGACCCAGGAAATGTGACCTGTTCGCG 1107
824 CAGTCGCGGGGCGCATGACATCTCAGGACTGATGTGACCCCTAGCCTCGGCTCTC 883
1108 CAGTCGCGGGGCGCATGACATCTCAGGACTGATGTGACCCCTAGCCTCGGCTCTC 1167
884 TTCATCGGCGCATTTCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCTAGTAAC 943
1168 TTCATCGGCGCATTTCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCTAGTAAC 1227
944 CCACTGAAGTGGCCAGAGGTTGCCACTGGCTGGATGCCAACACACACACACACACAG 1003
1228 CCACTGAAGTGGCCAGAGGTTGCCACTGGCTGGATGCCAACACACACACACACACAG 1287
1004 ATCTGCTAACTGCTCAGGCGCACTATCAGGACCAAGGTGATGGCTGTGTCACACAG 1063
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1304 CTCTGGAGTACCCGACCCCTGTTGAATATCACCAAGGAGGATACACCTTGTGGTGAG 1363
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RESULT 12

US-09-978-191A-253
; Sequence 253, Application US/09978191A
; Publication No. US20030050239A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918595
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; PRIOR FILING DATE: 1998-05-15

Query Match      51.1%; Score 1013; DB 10; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2,7e-292;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

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Db 388 GTTGCTTGACACACAGAGCCCTCAAGTGGTCAACAAATATGGAACCCCTGCAAGGAAA 447

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Db 448 CAGATGATGTGGGGAAGACACCCATCCAAAGTCTTTTAGAGTCCCTTCTCCAGACCT 507

Qy 344 CCTCTAGTATCCTCAGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 403
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Qy 404 GATGCTACCACTACCCGCCCTG----- 425
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Qy 426 ----- 425
Db 628 GCACGATCTGGCTCACTGCAACCTCCGCCCTCCGGGTTCAAGCGAGTCTCTGCCTCAG 687

Qy 426 -----GGTGCTGACAGAGTCCCTGGGCCAGCTGGCTCGATG 463
Db 688 CCTCTGAGTGTCTGGGGCTACAGTGTCTGACAGAGTCTCTGGGCCAGCTGGCTCGATG 747

Qy 464 TACGTACGACGCGGGAAACGTAACAAGTGGTGGCTTTCAGCGAGGACTGTCTGTACCTG 523
Db 748 TACGTACGACGCGGGAAACGTAACAAGTGGTGGCTTTCAGCGAGGACTGTCTGTACCTG 807

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Qy 584 CCGGAGGCGCTTTCATCTGTGGGCGCTTCTTTCGTACGAGGCTCTGACTTGGCGGCC 643
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Db 988 ACGACACAGCAGCAGCGCGCGGAACTGGGGGCTGTGGACAGATGGGGCTTCTCGC 1047
Qy 764 TGGGTGACGAGAAACATCGGAGCCTTCGGGGGAGACCCAGGAATGTGACCTTGTGGC 823
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Qy 1904 CCCTGGGAGACTAGCCATGACATACCTGGGACAGAGTCTTACCCA 1952
Db 1905 CCCTGGGAGACTAGCCATGACATACCTGGGACAGAGTCTTACCCA 1953

RESULT 13
US-09-978-403A-253
; Sequence 253, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: E2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22

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PRIOR APPLICATION NUMBER: 60/085697									
Query Match									
			51.1%;	Score 1013;	DB 10;	Length 2456;			

QY	224	GGTGCCTTGCACACCAAGAGGCGCTCAAGTGGTACCAAAATATGGAACCTGCAAGGAAA	283						
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QY	284	CAGATGATGTGGGAGAGACACCCATCAAGTCTTTTGGAGTCCCTTCTCCAGACCT	343						
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QY	344	CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA	403						
DB	508	CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA	567						
QY	404	GATGCTACCACTACCCGCGCTG	425						
DB	568	GATGCTACCACTACCCGCGCTG	627						
QY	426	-----	425						
DB	628	GCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTCAAGCGAGTCTCTCCCTCAG	687						
QY	426	-----GGTGCCTGAGAGTCTTGGGCGCAGCTGGCCCTGATG	463						
DB	688	CCTCTAGTGTCTGGGCTACAGGTGCTGAGGAGTCTTGGGCGCAGCTGGCCCTGATG	747						
QY	464	TACGTCACGACGCGGGAACGTTACAAGTGGCTCGCTTACGCGAGGACTGTCTGACCTG	523						
DB	748	TACGTCACGACGCGGGAACGTTACAAGTGGCTCGCTTACGCGAGGACTGTCTGACCTG	807						
QY	524	AACGTGTACG	583						
DB	808	AACGTGTACG	867						
QY	584	CCGGAGGCGCTTACGTCGGGCGCTCTTCTGTCAGAGGCTCTGACTTGGCCGCC	643						
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QY	644	CGCGAGAAAGTGGTCTGCTGTTCTGCGACACAGGCTCGGCATCTTCGGCTTCTGAGC	703						
DB	928	CGCGAGAAAGTGGTCTGCTGTTCTGCGACACAGGCTCGGCATCTTCGGCTTCTGAGC	987						
QY	704	ACGGAAGACGACGCGCGCGGGAACCTGGGGGCTGCTGGACAGATGGCGCTCTGCGC	763						
DB	988	ACGGAAGACGACGCGCGCGGGAACCTGGGGGCTGCTGGACAGATGGCGCTCTGCGC	1047						
QY	764	TGGGTGCAGGAGAACATCGACGCTTTCGGGGGAGACCCAGGAAATGTGACCTGTTCGCG	823						
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QY	824	CAGTCGGGGGGGCGCATGAGATCTCAGACTGATGATGTACCCCTAGCTCGGGTCTC	883						
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DB	1168	TTCCATCGGGCCATTTCCAGAGTGGCACCGGCTTATTCAGACTTTTTCATCACTAGTAAC	1227						
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DB	1228	CCACTGAAAGTGGCCAAAGAGGTTGCCACCTGGTGGATGCAACCAAGCAACAGCACAG	1287						
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DB	1288	ATCTGGTAACTGCTGAGGCACTATCAGGAGACCAAGGTGATCGGTGTGTCACCAAG	1347						
QY	1064	ATGAGATTCCTCAACTGAACCTTCAGAGAGACCCGGAAGATTTATCTGGTCCATGAGC	1123						
DB	1348	ATGAGATTCCTCAACTGAACCTTCAGAGAGACCCGGAAGATTTATCTGGTCCATGAGC	1407						
QY	1124	CCTGTGGTGGATGGTGTGTGATGCCAGATGACCTTTGGTCTCTCTGACCCAGGGGAG	1183						

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Qy 1184 GTTTCATCTGTCCTACCTCTAGGTGTCAACAACCTGGAATTCATTTGGCTCTTGSCCT 1243
Db 1468 GTTTCATCTGTCCTACCTCTAGGTGTCAACAACCTGGAATTCATTTGGCTCTTGSCCT 1527
Qy 1244 TATATCATGAAGTTCCTGCTAAACCGGAGCGGATGAGAAGAAACCATCACTAAGATG 1303
Db 1528 TAT 1530
Qy 1304 CTCTGGAGTACCCGACCCCTGTTGAATATCACCAGGAGGATACCATTTGTGTGGAG 1363
Db 1531 -----AATATCACCAGGAGGATACCATTTGTGTGGAG 1566
Qy 1364 GAGTACCTGGACATGTCATGACATGATGGAAGATGTACGAAACCGTATGATGGAC 1423
Db 1567 GAGTACCTGGACATGTCATGACATGATGGAAGATGTACGAAACCGTATGATGGAC 1626
Qy 1424 ATAGTTCAGATGCCACTTTGCTGTATGCCACCTGCGAGACTGCTCACTACCAACCGAT 1483
Db 1627 ATAGTTCAGATGCCACTTTGCTGTATGCCACCTGCGAGACTGCTCACTACCAACCGA--- 1683
Qy 1484 GCCGGCTCCCTGCTACCTGTATGAATTTGAGCACCAACCGCTGCTGGAATAATCGTCAAA 1543
Db 1684 ----- 1683
Qy 1544 CCCCCTGATGGGCGAGACCATGGGATGAGATGTACTTCTCTTTGGGGCCCCCTTC 1603
Db 1684 ----- 1683
Qy 1604 GCCACAGCCCTTTCATGGGTAAAGAGAGAGCCTTAGCCTCCAGATGATGAATACTGG 1663
Db 1684 ----- 1683
Qy 1664 GCCMACTTTGCCCGCAGAGAAACCCCAATGATGGGAATCTGCCCTGTGGCCACGCTAC 1723
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RESULT 14

US-09-978-564A-253

; Sequence 253, Application US/09978564A

; Publication No. US2003050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC25
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-03-31

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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      51.1%; Score 1013; DB 10; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.7e-292;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

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DB 448 CAGATGATGTGGGAAGACACCCATCCAAAGTCTTTTAGAGTCCCTTCTCCAGACCT 507
QY 344 CCTCTAGATATCCCTCAGTTTGTACCTCCAGAACCCCGGAGCCCTGGAAGAAATCAGA 403
DB 508 CCTCTAGATATCCCTCAGTTTGTACCTCCAGAACCCCGGAGCCCTGGAAGAAATCAGA 567
QY 404 GATGCTACCACTACCCGCGCTG----- 425
DB 568 GATGCTACCACTACCCGCGCTGAGTGTGCTCTGTGCGCAGGCTGGAGTGCAGTG 627
QY 426 ----- 425
DB 628 GCACGATCTCGGCTCACTGCAACCTCCCGCTCCCGGTTTCAAGCGAGTCTCTCGCTCAG 687
QY 426 -----GTTGCTCGAGAGTCTCTGGGCGAGCTGGGCTCGATG 463
DB 688 CCTCTGAGTGTCTGGGCGTACAGTGTCTGAGAGTCTCTGGGCGAGCTGGGCTCGATG 747
QY 464 TACGTACAGCAGCGGGGAACCGGTACAGTGTCTGGCTTTCAGCAGGAGTCTCTGTACCTG 523
DB 748 TACGTACAGCAGCGGGGAACCGGTACAGTGTCTGGCTTTCAGCAGGAGTCTCTGTACCTG 807
QY 524 AACGTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 583
DB 808 AACGTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 867
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DB 988 ACGGACGACAGCAGCGCGCGGAACTGGGGGCTGCTGGACACAGATGCGGCTGTGGC 1047
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DB 1048 TGGGTGACAGAGAACATGCGAGCTTTCGGGGAGACCCAGGAAATGTACCCCTGTTCGCG 1107
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QY 1004 ATCCTGCTAACTGCTTGGGGCACTATCAGGGACCAAGGTGATGCTGTGTCTTCCAAACAG 1063
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DB 1531 -----AATATCAACCAAGGAGAGGTACCACTTTGTTGGTGAAG 1566
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DB 1567 GAGTACCTGGCAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGAGC 1626
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DB 1725 AACAGGATGAAAGTACCTGCACTGGATTTTACCAAGAGTGGGCATGAAGCTCAAG 1784
QY 1784 GAGAAAGAGTGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAGACAGAGG 1843
DB 1785 GAGAAAGAGTGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAGACAGAGG 1844
QY 1844 CAATTCATAGGCTGGCTATGCAAGAGAGGCCAAAGAGGGTTTGGCCCCCACCACCTCAGG 1903
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QY 1904 CCCTGGGAGACTAGCCATGACATACCTCGGGACAGAGTCTTACCCA 1952
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Search completed: August 11, 2004, 22:36:09
Job time : 945.854 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 10:40:18 ; Search time 5212.08 Seconds
(without alignments)
11361.439 Million cell updates/sec

Title: US-10-001-227-1
Perfect score: 1983
Sequence: 1 ccttagccaattcgccga.....gtttaaactgcaggactag 1983

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: em_estba:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	900.4	45.4	3431 11 BC041823	BC041823 Homo sapi
3	825.4	41.6	988 12 EQ053090	EQ053090 AGENCOURT
4	761.2	38.4	1047 12 BM547028	BM547028 AGENCOURT

5	591.4	29.8	593 13 BQ269800	BQ269800
6	482.4	24.3	526 12 BI460262	BI460262 603201884
7	433	21.8	468 10 AW512144	AW512144 xus4e11.x
8	401.4	20.2	1918 14 CF111083	CF111083 Shultzomi
9	395	19.9	1944 11 AK078879	AK078879 Mus muscu
10	371.6	18.7	634 10 BB630313	BB630313 BB630313
11	363.8	18.3	403 9 AA450272	AA450272 zx42h02.r
12	346.6	17.5	478 14 CF1116765	CF1116765 ad555.z1
13	343	17.3	442 13 BX488287	BX488287 DKFZP866E
14	331.6	16.7	438 9 AI949486	AI949486 wq10h04.x
15	320	16.1	884 13 BX336837	BX336837 BX336837
16	319.2	16.1	710 10 BF126303	BF126303 601650490
17	319.2	16.1	1680 29 AY414459	AY414459 Homo sapi
18	309.8	15.6	881 13 BX397287	BX397287 BX397287
19	308.8	15.6	1438 14 CF111142	CF111142 Shultzomi
20	308.8	15.6	1438 14 CF111143	CF111143 Shultzomi
21	301.2	15.2	388 14 R85476	R85476 Y037809.sl
22	298.8	15.1	1680 29 AY414461	AY414461 Mus muscu
23	290.6	14.7	307 12 EG993190	EG993190 RC4-H1109
24	288.2	14.5	1050 10 BF236748	BF236748 602028044
25	285.2	14.4	2661 11 AK033563	AK033563 Mus muscu
26	283.6	14.3	2687 11 AK077248	AK077248 Mus muscu
27	274.8	13.9	1942 11 BC015286	BC015286 Mus muscu
28	270	13.6	731 12 BI761231	BI761231 603043472
29	266	13.4	1958 11 AK078953	AK078953 Mus muscu
30	264.8	13.4	4927 11 AK040349	AK040349 Mus muscu
31	264	13.3	731 13 EX095055	EX095055 BX095055
32	263.8	13.3	296 9 AA339398	AA339398 EST4476
33	261.8	13.2	412 10 BG013590	BG013590 CM4-GR036
34	259.6	13.1	621 9 AA865634	AA865634 og93h11.s
35	252.8	12.7	930 13 BQ716182	BQ716182 AGENCOURT
36	250	12.6	2038 11 EC019926	EC019926 Mus muscu
37	249	12.6	533 14 N44535	N44535 YY32C12.r1
38	239	12.1	257 10 BE831841	BE831841 RC6-M1006
39	231.6	11.7	650 14 CB468793	CB468793 734647 MA
40	231	11.6	904 13 BQ900930	BQ900930 AGENCOURT
41	228.2	11.5	472 14 N25091	N25091 YX18b11.r1
42	223.2	11.3	828 13 BQ900803	BQ900803 AGENCOURT
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44	221.2	11.2	900 13 BU164515	BU164515 AGENCOURT
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ALIGNMENTS

RESULT 1

AK037191

LOCUS

DEFINITION

Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched library, clone: A030007M20 product: hypothetical Carboxylesterases type-B containing protein, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AK037191 2356 bp mRNA linear HTC 19-SEP-2003
Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched library, clone: A030007M20 product: hypothetical Carboxylesterases type-B containing protein, full insert sequence.

AK037191 GI:26085654
HTC; CAP trapper.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.	QY	114	TGCCATCCACAGTGTGGCCATCACTCTGCCCCACAGCAGGAGCTGGCTGGAGCATGAGGT	173
AUTHORS		RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplex capillary sequencer	Db	44	TGACCCCAAGAGTGTAGGCATCACTGACAGCCCATGSCAAGCTGGTGGAAACATGAAGT	103
TITLE		Genome Res. 10 (11), 1757-1771 (2000)	QY	174	GGATTCTGTCTGGAGGCTCACTCCCTCTGCTGTATGGGGCAGACGGCTTGGGTGCTTGC	233
JOURNAL		20530913	Db	104	GGATTCTGGGCTTGGAGCTCACTCCCTGCTGTGTATGGAGTGTAGTCAGACAGCCTTAGGTGCTTTGC	163
MEDLINE		11076861	QY	234	ACACCAAGAGGCTCAAGTGTCTACCAAAATATGGAACCTGCAAGGAAAACAGATGATG	293
PUBMED			Db	164	ACACCAAGAGAACCTCTCTCTGATCACCACACAGGGATCTCTCAAGGAANGAAGTGCATG	223
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	QY	294	TGGGGAAGACACCCATCAAGTCTTTTATAGGAGTCCCTTCTTCCAGACCTCTCTCTAGGTA	353
AUTHORS		Nature 409, 685-690 (2001)	Db	224	TGGGAGACACACCCATCCCAAGTCTTCTCTGGGATCCCTTCTCTTAAACCTCCGGTGGGCA	283
TITLE		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	QY	354	TCTCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGAGATGCTACCA	413
JOURNAL		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Db	284	CCGCGAGTTTGTCTCTCCAGAGCCCGCTACCTTGGAAACGGCATCAGAGATGCCACCA	343
REFERENCE	5	Nature 420, 563-573 (2002)	QY	414	CCTACCCGCTGGGTGCTGAGAGTCTCTGGGGCCAGCTGGCTGATGTACGTACGTCAGCA	473
AUTHORS		6 (bases 1 to 2356)	Db	344	CCTACCCACCTTCGTGCTTCAGAAATCTCGGGGACAGATATATTATTCATCTTACCTTAACA	403
TITLE		Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, N., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T., Hori, F., Imozumi, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	QY	474	CGGGGAACGGTACAAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACTCGTAACCTGATG	533
JOURNAL		Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]	Db	404	CTCGGAACAGTATAAATGGCTGCATTTCACTGAGGACTGCGCTCTTACCTGAATGTGTATG	463
REFERENCE		Direct Submission	QY	534	CGCGGCGCGCGCGCGCGGGGATCCCGAGTCCCGAGTGTGTGTTTCCCGGAGGCG	593
AUTHORS		Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	Db	464	CCCAGTACTCGCCCCCTGGGGCCCTCTCTGCCAGTGTATGTTTGGTTCCTCGAGGTG	523
TITLE		Please visit our web site for further details.	QY	594	CTTTCATCTGTTGGGGCTGTCTTCTGTAGAGAGGCTGTGACTTGGCCCGCCGCGAGAAAG	653
JOURNAL		URL: http://genome.gsc.riken.go.jp/	Db	524	CTTTCCTCGCGGTTTCGGGTTTCCACTAGAAAGGCTCAGAGTTGGCGCCCGTGGGAAAG	583
COMMENT		URL: http://fantom.gsc.riken.go.jp/.	QY	654	TGTTGCTGTGTTTCTGACGACACAGGCTCGGCATCTTCGGGTTCTGAGCAGCAGCAGCA	713
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		1. 2356	Db	944	AATGCCTGAGGTCTCTCTCAGCAGAGGAGGTGACGCTTGTTCCTCAAGAGGATGTCATTCT	1003
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		Best Local Similarity 75.9%; Pred. No. 5.1e-241;	Db	1064	ATGCGTGTGTGTCCCAAGAGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1123
		Matches 1340; Conservative 0; Mismatches 423; Indels 3; Gaps 1;				

similar to SW:ES10_RAT P16303 LIVER CARBOXYLESTERASE 10 PRECURSOR
// mRNA sequence.
ACCESSION AW512144
VERSION AW512144.1 GI:7150222
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 468)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Prepared by: Life Technologies, Inc.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
image.llnl.gov/image/html/iresources.shtml
Possible reversed clone: similarity on wrong strand
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High quality sequence stop: 406.
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adenocarcinoma, 7 pooled tumors"
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Qy 551 GGGATCCCAAGCTGCCAGTGATGGTCTGGTTCCTGGGAGCGGCTTCATCGTGGCGCT 610
Db 121 GGGATCCCAAGCTGCCAGTGATGGTCTGGTTCCTGGGAGCGGCTTCATCGTGGCGCT 180
Qy 611 GCTTCTTCGTACGAGGGCTCTGACTTGGCGCGCGCGAGGAGTGGTGTCTGTTCTG 670
Db 181 GCTTCTTCGTACGAGGGCTCTGACTTGGCGCGCGCGAGGAGTGGTGTCTGTTCTG 240
Qy 671 CAGCACAGGCTCGGCATCTTCGGGTTCTGTAGCAGGACGACACGCCACGCGCGCGGAG 730
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Qy 731 TGGGGGCTGTGGACAGATCGGCGCTTCGGCTTCGGTTCGTAGGAGACATCGAGCGCTTC 790
Db 301 TGGGGGCTGTGGACAGATCGGCGCTTCGGCTTCGGTTCGTAGGAGACATCGAGCGCTTC 360
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Db 361 CGGGAGACCCAGCAATGACCTTTGGCAGTCGGCGGGGCGCATGAGCATCTCA 420
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Db 421 GGAATGATGATGACCCCTAGCTGGGTCTTTCATCGGCGCATTTCC 468
RESULT 8
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LOCUS Shultscomica04334 Rat lung airway and parenchyma cDNA libraries
DEFINITION Rattus norvegicus cDNA clone Contig3845 5', mRNA sequence.
ACCESSION CF111083
VERSION CF111083.1 GI:33167595
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
1 (bases 1 to 1918)
Shultz, M.A., Zhang, J., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V.,
Padua, A.M., Gurske, W.A., Morin, D., Penn, S.G., Jovanovich, S.B.,
Plopper, C.G. and Buckpitt, A.R.
Gene Expression Analysis in Response to Lung Toxicants: I.
Sequencing and Microarray Development
Unpublished (2003)
Contact: Shultz, MA
Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 0793
Fax: 530 752 4698
Email: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred <
20) and vector/linker sequence has been removed.
High quality sequence stop: 1918.
Location/Qualifiers
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Db 176 GTTTCCTGGGAATCCCTTCGCCAAGTCCCTCTGGCTCTCTGAGTTTGTCTCA 235
Qy 374 GAACCCCGGAGCCCTGGAAAGATCAGAGTGTACACCTACCCGCTGGGTGCTG 433
Db 236 CAGCCTGACAGTCTTGGAACTTTGTGAAGATATCTCTCTACCCACCTATGTCT 295
Qy 434 CAGGAGTCTCTGGGGCCAGCTGGCTGTGATGTACGTACGACGCGGGAACGGTACAG 490
Db 296 CAAGATGCTGTTGGAGGGCAGGTTCTCTCAGAGCTTTTCCACACAGGAAGAAACATT 355
Qy 491 TGGCTCGGTTTCAGGAGGAGTGTCTGTACCTGAACGTCTACGCGCGCGCGGCC 550
Db 356 CCTTTACAGTTTCTTGAAGACTGCCTTACCTGAAATGTTTACTCCCGCTACTTGACA 415

QY 551 GGGGATCCCGAGCTGCGAGTGTGTTGTTCCCGGAGCGCGCTTTCATCGTGGGCGCT 610
Db 416 AAGAACACCGCGTTTACAGTGTGTTGATCCATCGAGTGGTGTAGTGGTGA 475
QY 611 GCTTCTTGTTGACGAGGCTCTGACTTGGCCCGCCCGAGAAAGTGTGCTGTTGTTCTG 670
Db 476 TCATCCACTATGATGACAGCGCTCTCTGCGCATGAAATGTGTGGTGGTGAACATT 535
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QY 1628 GAGAAAGGCACTTAGCTCCAGATGATGAATACTGGGCAAACTTTGCCCGCACAGGAAC 1687
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RESULT 9
AK078879
LOCUS
DEFINITION
AK078879 1944 bp mRNA linear HTC 18-SEP-2003
Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030604P03 product:carboxylesterase 3, full insert sequence.
ACCESSION
AK078879.1 GI:26347580
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493374
11042159

3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1944)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tanami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source

1..1944
/organism="Mus musculus"
/mol_type="mRNA"
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1922..1927
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1944
/note="putative"

polyA_signal

polyA_site

ORIGIN

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Matches 830; Conservative 0; Mismatches 655; Indels 12; Gaps 3;

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DB 208 GTTTCCTGGAGTCCCTTTGCCAGCCCTCTTGCTCCTTGAGATTGCTCCACCA 267
QY 374 GAACCCCGGAGCCCTGGAAGGAATCAGAGATCTACCACTACCGCTGGGTGCTG 433
DB 268 CAGCTGCAGAGCCCTGGAGCTTGCTGAAGAACCACTCTCTACCGCCCTATGTGCTCT 327
QY 434 CAGGATC---CTGGGGCCAGCTGGCTCGATGTACGTACGACGCGGGAACGTTACAG 490
DB 328 CAGGATGTGTGGAGGCGGTGCTCTCAGAGCTCTCTACCACTCTTCCAAACAGGAAGAACATT 387

491 TGGTGGCGCTTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCGCGCGCGCGCGCC 550
388 CTTTACAGTTTTTCTGAGACTGCTCTACTCTGAATTTTACACTCTCTGCTGACTTGACA 447
QY 551 GGGGATCCCCAGCTGCCAGTGATGGTGTGCTCCGGAGGCGCTTTCATCGTGGGCGCT 610
DB 448 AAGAACAGCAGACTACCAGTGATGGTGTGATCCATCCAGGTGAGCTGGTGGCGGGA 507
QY 611 GCTTCTTCTGACGAGGCTCTGACTTGGCGCGCGCGAGAAAGTGGTCTGCTGTTTCTG 670
DB 508 GATCCACTATGATGGACTGGCCCTCTCTGCCATGAAATGTGGTGGTGGTGAACATT 567
QY 671 CAGCAGAGCTCGGCATCTTCGGTTCCTGAGCAGGACGACAGCCAGCGCGCGGGAAC 730
DB 568 CAGTATCGCTTGGCATCTGGGGATTTCTCAGCACTGGGGATGAACAACAGTCGGGGAAC 627
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DB 698 GGGGCAACCCAGGCTCGTGCACCATCTTGGAGATCAGCAGGAGGTTTTCAGTGTCTCT 747
QY 851 GGACTGATGATGTACCCCTAGCTCGGTCTCTTCGATCGGCGCATTTCCAGAGTGGC 910
DB 748 GTTCTGTCTTGTCTCTTTGCGCAAGAACCTTCCACAGGGCAATTTTCAGAGTGGT 807
QY 911 ACCGGTATTTCAGACTTTTTCATCACTAGTAGTAAACCACTGAAAGTGGCCAAAGAGTTGCC 970
DB 808 GTGTCCCTCAGCTGCTCTGATTACACAGATGTAAAGCCCATTTGCTGGTGTGCT 867
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DB 928 ACAGAGGATGAACACTACTGAGACCTCACTAAATTTGAATCTTTTAACTGCACTTACTT 987
QY 1091 AGAGACCCGGGAAGAGATTATCTGGTTCATGAGCCCTGTGGTGGATGGTGTGGTATCCCA 1150
DB 988 GGAATTCAAAAGAGAGCTATCCCTTCTCTCTCTGATTGATGAGAGTAGTTCTGCGCA 1047
QY 1151 GATGACCTTTGGTCTCTGACCCAGCGGGAAGTTTTCATCTGTGCCCTACTCTTAGT 1210
DB 1048 AAGGCACCAAGAGAGATCTGCTGAGAAGAGTTTCAGACCTGTCCCTACATAGTGGC 1107
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DB 1108 ATCAACNAGCAAGAGTTTGGCTGGATCATTCACACGCTTATGGGCTATCCACTCGCTGAA 1167
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QY 1451 GCCACACTGCAGACTGCTCACTACCAACGAGATGCGGCCCTCCCTGCTTACCTGTATGAA 1510
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DB 1402 TTTGAGTATCGCCCAAGCTTTTGTATCGGCCATGAGACCCCAAGGCAAGTAATAGAGACCAAT 1461
QY 1568 GGGGATGAGATGTACTTCTCTTTGGGGCCCCCTTCGCCACAGGCTTTTCCATGGGTAG 1627


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RESULT 11
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LOCUS      zx4202.r1 Soares_total_fetus Nb2HF8.9; Homo sapiens cDNA clone
DEFINITION      IMAGE:789171.5, similar to IR:GI931_G1931 CARBOXYPEPTIDASE
PRECUSOR      ; mRNA sequence.
ACCESSION      AA450272
VERSION      AA450272.1 GI:2164022
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 403)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Scheinberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
TITLE      Unpublished (1997)
JOURNAL      Contact: Willson RK
COMMENT      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLMU ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Source      1..403
             /organism="Homo sapiens"
             /mol_type="mRNA"
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             /clone_lib="Soares total fetus Nb2HF8.9w"
             /notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - gligo(dT) primer [5',
TGTTACCACTGAAGTGGAGCGCGCTTAATTTTATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match      18.3%; Score 363.8; DB 9; Length 403;
Best Local Similarity 97.7%; Pred. No. 1.4e-74;
Matches 390; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
QY      858 TGATGTCAACCCCTAGCTCGGGTCTCTTCATCGGGCCATTCGCCAGTGGCAACCGCT 917
DB      1 TGATGTCAACCCCTAGCTCGGGTCTCTTCATCGGGCCATTCGCCAGTGGCAACCGCT 60
QY      918 TATTCAGACTTTTCATCACTAGTAACCCACTGAAGTGGCCAGAGGTTGCCACCTGG 977
DB      61 TGTTCAAGACTTTTCATCACTCGTAACCCACTGAAGT-GCCAGAGGTTGCCACCTGG 119
QY      978 CTGGATGCAACCAACACAGCACACAGATCTCTGGTAAACTGCCTGAGGCGCACTATCAGGGA 1037
DB      120 CTGGATGCAACCAACACAGCACACAGATCTCTGGTAAACTGCCTGA-GGCACATCAGGGA 178
QY      1038 CCAGGTGATCGGTGTCTCCAAAGATGAGATTCCTCCAACTCAACTTCAGAGAGACC 1097
DB      179 CCAGGTGATCGGTGTCTCCAAAGATGAGATTCCTCCAACTCAACTTCAGAGAGACC 238
QY      1098 CGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTATCCAGATGACC 1157

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DB      239 CGGAAGAGATTATCTGGTCCAAGAGCCCTGTGGTGGATGGTGTGGTATCCAGATGACC 298
QY      1158 CTTTGGTGCTCTCTGACCCAGGGGAAGGTTTCATCTGTGCGCTACCTTCTAGGTCTCAACA 1217
DB      299 CTTTGGTGCTCTCTGACCCAGGGGAAGGTTTCATCTGTGCGCTACCTTCTAGGTCTCAACA 358
QY      1218 ACCTGGAATTCGAATGGCTCTTGTCTTATATCATGAAGT 1256
DB      359 ACCTGGAATTCGAATGGCTCTTGTCTTATGAATGAGT 397

RESULT 12
CF116765      478 bp      mRNA      linear      EST 23-JUL-2003
LOCUS      ad555.z1 ad adult sheep skin library Ovis aries cDNA, mRNA
DEFINITION      sequence.
ACCESSION      CF116765
VERSION      CF116765.1 GI:33179023
KEYWORDS      EST.
SOURCE      Ovis aries (sheep)
ORGANISM      Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE      1 (bases 1 to 478)
AUTHORS      Desilva,U., Franklin,I.R., Maddox,J.F., van Hest,B. and
Adelson,D.L.
Gene Expression in Sheep Skin and Wool (Hair)
Cytochrome. Genome Res. (2003) In press
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
FEATURES
Source      1..478
             /organism="Ovis aries"
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EcoRI; Site 2: XbaI; Arrayed library filters screened by
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strand synthesis XbaI-(dT)15 primed, EcoRI adaptors were
ligated to cDNA before cloning. EcoRI- NotI- SalI adaptor
sequence; 5'-AATTCGGCGCGCTCGAC GCGCGGCGAGCTG-P04-5' 5'
sequencing primer 5' TCGAGATCTGGAGAGC 3' 3' sequencing
primer 5' TATACGACTCACTATAGG 3' submitted sequences in
excess of 50 bp after vector and quality clipping(phred
13) submitted to GenBank."
ORIGIN
Query Match      17.5%; Score 346.6; DB 14; Length 478;
Best Local Similarity 84.1%; Pred. No. 1.7e-70;
Matches 391; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY      307 CATCAAGTCTTTTATAGAGTCCCTTCTCCAGACTCTCTAGTATCTCTAGGTTTGC 366
DB      14 CATCAATGTCTCTAGGAGTTCCCTTCTCCAGACTCTCTAGGTTTGC 73
QY      367 ACCTCCAGAACCCCGGAGCCCTGGAAGGATCAGATGCTACACCTACCCGCTGG 426
DB      74 TGCCCCAGAACCCCGGAGCCCTGGAAGGATCAGATGCTACACCTATGCCCTGT 133
QY      427 GTGCCCTGCAAGAGTCTCTGGGGCCAGCTGGCTTCGATGTACGTACAGCCGGGAACGGTA 486

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Db 134 GTGGCTCAGAGTCTGGGGGAGGTCACCTCACTATTTCACACACGCGAGCAT 193

Qy 487 CAAGTGGCTGGCTTACGAGGAGTCTGTGTACCTGAACGTGTACGCGCGGCGCGC 546

Db 194 TAAATGGCTGCACCTCAATGAGGAGTCTGTACCTGAATGTGCACGCGCCAGTGGAGC 253

Qy 547 GCGCGGGATCCAGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 606

Db 254 GCGCGGGACCTCTGAGCGCGGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 313

Qy 607 CGCTGCTCTTCTGACAGGAGTCTGACCTTGGCGCGCGCGCGAGAAAGTGTGTGTGT 666

Db 314 TTCCGCTTCCAGTACGATGCTCCGATTTGGCTGCTCCGCGGAGAAAGTGTGTGTGT 373

Qy 667 TCTGACAGCAGGCTCGGATCTTTCGCTTCTGAGCAGCAGCAGCAGCAGCAGCAGCAG 726

Db 374 TCTGACAGCAGGCTCGGATCTTTCGCTTCTGAGCAGCAGCAGCAGCAGCAGCAGCAG 433

Qy 727 GAACTGGGGGCTGTGACAGAGTGGCGGCTGTGCGCTGGGTGCA 771

Db 434 GAACTGGGGGCTGTGACAGAGTGGCGGCTGTGCGCTGGGTGCA 478

RESULT 13

LOCUS BX488287

DEFINITION DKFZp686E07269 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

ACCESSION BX488287

VERSION BX488287.1 GI:31953725

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 442)

AUTHORS Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

TITLE EST (Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., et al.)

JOURNAL Unpublished (2003)

COMMENT Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

No si' sequence available.

This clone (DKFZp686E07269) is available at the R2PD in Berlin.

Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@r2pd.de.

FEATURES

source

1..442

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/clone="DKFZp686E07269"

/dev_stage="adult"

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/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

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Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 GTGGCTGAGGAGTCTGGGGGAGGTCACCTCACTATTTCACACACGCGAGCAT 485

Db 100 GTGGCTGAGGAGTCTGGGGGAGGTCACCTCACTATTTCACACACGCGAGCAT 159

Qy 486 ACAAGTGGCTGGCTTACGAGGAGTCTGTGTACCTGAACGTGTACGCGCGGCGCGC 545

Db 160 ACAAGTGGCTGGCTTACGAGGAGTCTGTGTACCTGAACGTGTACGCGCGGCGCGC 219

Qy 546 GCGCGGGATCCAGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 605

Db 220 GCGCGGGATCCAGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 279

Qy 606 GCGCTGCTTCTTCTGACAGGAGTCTGACCTTGGCGCGCGCGAGAAAGTGTGTGTGT 665

Db 280 GCGCTGCTTCTTCTGACAGGAGTCTGACCTTGGCGCGCGCGAGAAAGTGTGTGTGT 339

Qy 666 TTCTGACAGCAGGCTCGGATCTTTCGCTTCTGAGCAGCAGCAGCAGCAGCAGCAGCAG 725

Db 340 TTCTGACAGCAGGCTCGGATCTTTCGCTTCTGAGCAGCAGCAGCAGCAGCAGCAGCAG 399

Qy 726 GAACTGGGGGCTGTGACAGAGTGGCGGCTGTGCGCTGGGT 768

Db 400 GAACTGGGGGCTGTGACAGAGTGGCGGCTGTGCGCTGGGT 442

RESULT 14

LOCUS AI949486/c

DEFINITION AI949486 438 bp mRNA linear EST 08-MAR-2000

similar to SW:SASB_ANAPL_Q04791 FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN ;, mRNA sequence.

ACCESSION AI949486

VERSION AI949486.1 GI:5741718

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 438)

AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: CGAPBS-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LBNL at: www.bio.lnlni.gov/bbrp/image/image.html

Insert Length: 498 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 330.

Location/Qualifiers

1..438

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/db_xref="taxon:9606"

/clone="IMAGE:2470903"

/tissue_type="2 pooled tumors (clear cell type)"

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/clone_lib="NCI-CCAP_Kid12"

/note="Organ: kidney; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; Plasmid DNA from the normalized library NCI-CCAP_Kids was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN


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Query Match
Best Local Similarity 16.7%; Score 331.6; DB 9; Length 438;
Matches 334; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 89 ACGGCTACCATGCCATCCACAGTGTCCATCCACAGTGTGGCCATCCTCTGCCACA 148
DB 434 ACGGCTACCATGCCATCCACAGTGTTCGCCATCCACAGTGTGGCCATCCTCTGCCACA 375
QY 149 GCAGGAGCTGGCTGGAGCATGAGTGATCTCTGCTGGAGGCTCACCCTCTGCCGTATG 208
DB 374 ACAGGAGCTGGCTGGAGCATGAGTGATCTCTGCTGGAGGCTCACCCTCTGCCGTATG 315
QY 209 GCGCAGACGGGCTTTGGGTGCTTCCACACCAAGAGGCTCAAGTGTGTCAACCAATATGGA 268
DB 314 GCGCAGACGGGCTTTGGGTGCTTCCACACCAAGAGGCTCAAGTGTGTCAACCAATATGGA 255
QY 269 ACCCTGCAAGAAACAGATGTCATGTGGGAAGACACCCATCCAACTCTTTTAGGATC 328
DB 254 ACCCTGCAAGAAACAGATGTCATGTGGGAAGACACCCATCCAACTCTTTTAGGATC 195
QY 329 CCCTTCTCCAGACCTCCTCTAGGTATCCTCAGGTTCGACCTCCAGAACCCCGGAGCCC 388
DB 194 CCCTTCTCCAGACCTCCTCTAGGTATCCTCAGGTTCGACCTCCAGAACCCCGGAGCCC 135
QY 389 TGGAAAGGAATCAGAGATGCTACCACTACCCGCTGG 426
DB 134 TGGAAAGGAATCAGAGATGCTACCACTACCCGCTGG 97

RESULT 15
BX336837 884 bp mRNA linear EST 01-MAY-2003
DEFINITION BX336837 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI033YE23 5-PRIME, mRNA sequence.
ACCESSION BX336837
VERSION BX336837.1 GI:30308514
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 884)
Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8153.f,
Contact : Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI033AC12QF1.
FEATURES
Location/Qualifiers
1..884
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match
Best Local Similarity 16.1%; Score 320; DB 13; Length 884;
Matches 403; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

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QY 1477 CCGAGATGCCGGCCTCCCTGTCTACTGTATGAATTTGAGCACCACGCTCGTGAATAT 1536
DB 109 CCGAGATGCCGGCCTCCCTGTCTACTGTATGAATTTGAGCACCACGCTCGTGAATAT 168
QY 1537 COTAAACCCCGCACTGATGGGGCAGACCATGGGGATGAGATGTACTTCTCTTTGGGG 1596
DB 169 COTAAACCCCGCACTGATGGGGCAGACCATGGGGATGAGATGTACTTCTCTTTGGGG 228
QY 1597 CCCCTTTCGCCACAGGCCCTTTCCATGGGTAAGAGAAGGCACCTTAGCCTCCAGATGAA 1656
DB 229 CCCCTTTCGCCACA----- 241
QY 1657 ATACTGGGCCAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGTGCCC 1716
DB 242 -----GAAACCCCAATGATGGGAATCTGCCCTGTGCCC 275
QY 1717 ACGCTACACACAGGATGAAAGTACCTCGAGCTGGATTTTACCACAAGAGTGGGCATGAA 1776
DB 276 ACGCTACACACAGGATGAAAGTACCTCGAGCTGGATTTTACCACAAGAGTGGGCATGAA 335
QY 1777 GCTCAAGGAGAGAAGATGGCTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTTGAGAA 1836
DB 336 GCTCAAGGAGAGAAGATGGCTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTTGAGAA 395
QY 1837 GCAGAGGCAATTTCTAAGGTGCTATGCAGGAGGAGCCAAAGAGGGGTTTGGCCCCCACC 1896
DB 396 GCAGAGGCAATTTCTAAGGTGCTATGCAGGAGGAGCCAAAGAGGGGTTTGGCCCCCACC 455
QY 1897 ATCCAGGGCCCTGGGGAGAGTAGCCATGGACATACCTGGGGACAAGAGTTCTTACCCA 1952
DB 456 ATCCAGGGCCCTGGGGAGAGTAGCCATGGACATACCTGGGGACAAGAGTTCTTACCCA 511

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Search completed: August 11, 2004, 18:13:28
Job time : 5231.08 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 22:23:05 ; Search time 57 Seconds

(without alignments)
2894.873 Million cell updates/sec

Title: US-10-001-227-2

Perfect score: 3112
Sequence: 1 MPSTVLFSTVLPSSLPTAGA.....KMAFWMSLYQSQRPEKQRF 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep_29Jan04:*

- 1: Genesep1980s:*
- 2: Genesep1980s:*
- 3: Genesep2000s:*
- 4: Genesep2001s:*
- 5: Genesep2002s:*
- 6: Genesep2003as:*
- 7: Genesep2003bs:*
- 8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3112	100.0	584	5	ABb79484 Human car
2	3112	100.0	584	5	AAe21052 Human dru
3	2391.5	76.8	509	4	ABg10635 Novel hum
4	2026.5	65.1	545	2	AAy41723 Human PRO
5	2026.5	65.1	545	4	AAu29052 Human PRO
6	2026.5	65.1	545	6	ABu58428 Human PRO
7	2026.5	65.1	545	6	ABu87976 Novel hum
8	2026.5	65.1	545	6	ABu84291 Human sec
9	2026.5	65.1	545	6	ABr66165 Human sec
10	2026.5	65.1	545	6	ABr65555 Human sec
11	2026.5	65.1	545	6	ABu99495 Human sec
12	2026.5	65.1	545	6	ABu82734 Human PRO
13	2026.5	65.1	545	6	ABu89855 Novel hum
14	2026.5	65.1	545	6	ABr68104 Human sec
15	2026.5	65.1	545	6	ABu96157 Novel hum
16	2026.5	65.1	545	6	ABu92588 Human sec
17	2026.5	65.1	545	6	ABo08665 Human sec
18	2026.5	65.1	545	6	ABc02717 Human sec
19	2026.5	65.1	545	6	ABr74871 Human sec
20	2026.5	65.1	545	6	ABr94633 Human sec
21	2026.5	65.1	545	6	ABc025225 Novel hum
22	2026.5	65.1	545	6	ABu85606 Human PRO
23	2026.5	65.1	545	6	ABu98766 Novel hum
24	2026.5	65.1	545	6	ABu97981 Novel hum
25	2026.5	65.1	545	6	ABu91687 Novel hum

26	2026.5	65.1	545	6	ABU72231	Novel hum
27	2026.5	65.1	545	6	ABU89380	Human PRO
28	2026.5	65.1	545	6	ABU86221	Human sec
29	2026.5	65.1	545	6	ABU67434	Human sec
30	2026.5	65.1	545	6	ABU80462	Human PRO
31	2026.5	65.1	545	6	ABR99380	Human sec
32	2026.5	65.1	545	6	ABR98770	Human sec
33	2026.5	65.1	545	6	ABO16293	Human sec
34	2026.5	65.1	545	6	ABR92193	Human sec
35	2026.5	65.1	545	6	ABO18834	Human sec
36	2026.5	65.1	545	6	ABR78255	Human sec
37	2026.5	65.1	545	6	ABU84991	Novel hum
38	2026.5	65.1	545	6	ABO00130	Novel hum
39	2026.5	65.1	545	6	ABO11462	Human sec
40	2026.5	65.1	545	6	ABO02107	Human sec
41	2026.5	65.1	545	6	ABU88681	Novel hum
42	2026.5	65.1	545	6	ABU83376	Human sec
43	2026.5	65.1	545	6	ABO06177	Novel hum
44	2026.5	65.1	545	6	ABR59213	Human sec
45	2026.5	65.1	545	6	ABO09275	Human sec

ALIGNMENTS

RESULT 1
ID ABB79484 standard; protein; 584 AA.
XX
AC ABB79484;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human carboxylesterase-2 (COE-2).
XX
KW Carboxylesterase-2; COE-2; human; antiinflammatory; virucide; antiulcer;
KW antiasthmatic; antirheumatic; antiarthritic; dermatological;
KW antipsoriatic; analgesic; antitumour; cytostatic; enzyme; gene therapy.
XX
OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Domain	25..569
FT		/note= "Carboxylesterase domain"
FT	Domain	26..45
FT		/note= "Transmembrane domain"
FT	Domain	44..158
FT		/note= "type-B similar family carboxylesterase/ lipase domain"
FT	Domain	52..115
FT		/note= "carboxylesterase precursor domain"
FT	Region	137..147
FT		/note= "Carboxylesterase type B2 signature motif"
FT	Domain	144..246
FT		/note= "hydrolase lipase hormone-sensitive lipid degradation domain"
FT	Region	231..246
FT		/note= "Carboxylesterase type B1 signature motif"
FT	Domain	245..263
FT		/note= "Transmembrane domain"
FT	Domain	249..308
FT		/note= "type-B similar family carboxylesterase/ lipase domain"
FT	Domain	254..340
FT		/note= "Carboxylesterase family multigene reticulum hydrolase signal domain"
FT	Domain	254..332
FT		/note= "Glycoprotein serine carboxylesterase acetylcholinesterase cocaine B-esterase domain"
FT	Domain	360..542
FT		/note= "Esterase hydrolase p-nitrobenzyl polyurethane domain"
FT	Domain	364..577

FT /note= "esterase carboxylase serine alpha esterase
FT domain"
FT 366..474
FT /note= "carboxylesterase signal serine liver glycoprotein
FT domain"
FT 395..554
FT /note= "acetylcholinesterase domain"
FT 415..573
FT /note= "esterase domain"
FT 487..569
FT /note= "esterase hydrolase domain"
FT 536..580
FT /note= "carboxylesterase hydrolase precursor domain"
FN WO200244357-A2.
XX
XX 06-JUN-2002.
XX 30-NOV-2001; 2001WO-US045356.
XX 30-NOV-2000; 2000US-0250929P.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kapeller-Libermann R, Silos-Santiago I;
XX WPI; 2002-537452/57.
XX N-PSDB; ABN84189.
XX Novel isolated human carboxylesterase-2 family member polypeptide, 18903,
XX useful for treating inflammatory disorders, pain disorders, tumor and
XX cancer.
XX
XX Claim 12; Page 122-123; 129pp; English.
XX
XX The present sequence is the protein sequence of human carboxylesterase-2
XX (COE-2), a novel carboxylesterase family member. COE-2 participates in
XX the metabolism of various lipid and fatty acid compounds which are
XX involved in pain and/or inflammation signalling. It is highly expressed
XX in tissues which contain afferent neurons, particularly brain and spinal
XX cord tissue. Homology searches against different databases identified a
XX number of characteristic domains and motifs in the COE-2 amino acid
XX sequence. The invention provides COE-2 nucleic acid molecules, antisense
XX nucleic acid molecules, recombinant expression vectors, host cells,
XX transgenic animals, isolated COE-2 proteins, fusion proteins, antigenic
XX peptides and anti-COE-2 antibodies. COE-2 binding substances are used in
XX claimed methods of identifying subjects having, or at risk of developing,
XX an inflammatory or pain disorder. Compounds capable of treating an
XX inflammatory or pain disorder are identified from their ability to
XX modulate COE-2 nucleic acid expression or COE-2 polypeptide activity.
XX Modulator compounds are used in a claimed method of treating an
XX inflammatory or pain disorder. Carboxylesterase-associated pain disorders
XX include hyperalgesia, pain associated with musculoskeletal disorders and
XX pain associated with surgery, rheumatoid arthritis, viral infection,
XX allergic reaction, asthma, pancreatitis, somatoform disorders,
XX fibromyalgia syndrome, etc. Carboxylesterase-associated inflammatory
XX disorders include viral infection, ulcerative colitis, Crohn's disease,
XX asthma, rheumatoid arthritis, scleroderma, psoriasis, inflammatory bowel
XX disorder, peritonitis, chronic obstructive pulmonary disease, lung
XX inflammation, asthma, appendicitis, septic shock, nephritis, amyloidosis,
XX chronic bronchitis, sarcoidosis, scleroderma, lupus, polymyositis,
XX Reiter's syndrome, psoriasis, pelvic inflammatory disease, inflammatory
XX breast disease, orbital inflammatory disease. Other carboxylesterase-
XX associated disorders include tumours, cancer, aberrant blood pressure,
XX aberrant blood clotting, misregulation of various reproductive functions
XX e.g. induction of labour, and misregulation of the sleep/wake cycle. COE-
XX 2 nucleic acids and polypeptides are also useful in screening assays,
XX detection assays (e.g., chromosomal mapping, tissue typing, forensic
XX biology) and predictive medicine (e.g., diagnostic assays, prognostic
XX assays, monitoring clinical trials and pharmacogenomics)
XX
XX Sequence 584 AA;

Query Match 100.0%; Score 3112; DB 5; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.9e-286;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPSTVLPSLPSLPTAGAGSMRWILCWSLTLCLMAQTALGALHTKRPQVTKYGLQ 60
DB 1 MPSTVLPSLPSLPTAGAGSMRWILCWSLTLCLMAQTALGALHTKRPQVTKYGLQ 60
QY 61 GKQMHVGTPIQVFLGVFSPPLGILFAPPEPEPWKGIKRDATTYPGCLQSWGOLA 120
DB 61 GKQMHVGTPIQVFLGVFSPPLGILFAPPEPEPWKGIKRDATTYPGCLQSWGOLA 120
QY 121 SMYVSTRERYKWLRESEDCLYLVYAPAPAGDQPLPVWVWFGAFVGAASVEGSD 180
DB 121 SMYVSTRERYKWLRESEDCLYLVYAPAPAGDQPLPVWVWFGAFVGAASVEGSD 180
QY 181 AAREKVLVFLQHLRIGFGLSTDDSHARGNGLLDQMAALRWVQENIAAFGGP 240
DB 181 AAREKVLVFLQHLRIGFGLSTDDSHARGNGLLDQMAALRWVQENIAAFGGP 240
QY 241 FQSSAGANSISGLMWSPLASGLFHRASQSGTALFRLPITSNPLKVAHVLAHCNHS 300
DB 241 FQSSAGANSISGLMWSPLASGLFHRASQSGTALFRLPITSNPLKVAHVLAHCNHS 300
QY 301 TQILVNCILRALSGLTKMVRVSNKMRFLQLNFORDPEEIIWMSPVVDGVIPDD 360
DB 301 TQILVNCILRALSGLTKMVRVSNKMRFLQLNFORDPEEIIWMSPVVDGVIPDD 360
QY 361 GKVSVPYLLGVNNLEFNWLLPYIMKPLNQARKEKITIKMLWSTRLNITKEQVPLV 420
DB 361 GKVSVPYLLGVNNLEFNWLLPYIMKPLNQARKEKITIKMLWSTRLNITKEQVPLV 420
QY 421 VEEYLDNNEHDKMLRNRMMDIVQDATFVYATQTAHYHRDAGLPVLYVEFEHARGII 480
DB 421 VEEYLDNNEHDKMLRNRMMDIVQDATFVYATQTAHYHRDAGLPVLYVEFEHARGII 480
QY 481 VKPRTGDAGHDGEMVYFLGGPFATGLSNGKEKALSQMKYKWNFARTNPNDGNLPCWP 540
DB 481 VKPRTGDAGHDGEMVYFLGGPFATGLSNGKEKALSQMKYKWNFARTNPNDGNLPCWP 540
QY 541 RYNKDEKYLQDFTTRVGMKLEKKAFAWMSLYQSQRPEKORQF 584
DB 541 RYNKDEKYLQDFTTRVGMKLEKKAFAWMSLYQSQRPEKORQF 584
★
RESULT 2
AAE21052
ID AAE21052 standard; protein; 584 AA.
XX AAE21052;
AC AAE21052;
XX
XX 01-JUL-2002 (first entry)
DE Human drug metabolising enzyme (DME-10) protein.
KW Human; drug metabolising enzyme; cell proliferative disorder; metabolic;
KW autoimmune; inflammatory; developmental; gastrointestinal; hypergonadal;
KW pancreatic; endocrine; eye; dermatitis; Addison's disease; antileptemic;
KW acquired immunodeficiency syndrome; AIDS; glomerulonephritis; anorectic;
KW diabetes; atherosclerosis; adult respiratory distress syndrome; anaemia;
KW Grave's disease; thyroiditis; Crohn's disease; infection; anticoagulant;
KW systemic lupus erythematosus; cirrhosis; psoriasis; epilepsy; gastritis;
KW cataract; hypopituitarism; cancer; rheumatoid arthritis; conjunctivitis;
KW cystic fibrosis; peptic ulcer; Wilson's disease; hepatitis; antithyroid;
KW allergy; diarrhoea; thrombosis; obesity; immunosuppressant; tranquilizer;
KW infertility; vulvare; anticonvulsant; gynaecological; laxative; goitre;
KW neutropenic; jaundice; trauma; asthma; DME-10; enzyme.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..43
XX /label= Signal_peptide
FT

FT Protein 44..584
 FT /note= "Mature human DME-10 protein"
 FT Domain 137..147
 FT /note= "Carboxylesterase B2 motif"
 FT Domain 231..246
 FT /note= "Carboxylesterase B1 motif"
 XX WO200212467-A2.
 XX 14-FEB-2002.
 XX 03-AUG-2001; 2001WO-US024382.
 XX 04-AUG-2000; 2000US-0223055P.
 XX 11-AUG-2000; 2000US-0224728P.
 XX 18-AUG-2000; 2000US-0226440P.
 XX 24-AUG-2000; 2000US-0228067P.
 XX 31-AUG-2000; 2000US-0230063P.
 XX 13-SEP-2000; 2000US-0232244P.
 XX 20-SEP-2000; 2000US-0234269P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Baughn MR, Bruns CM, Das D, Delegeane AM, Ding L, Elliott VS;
 PI Gandhi AR, Griffin JA, Hafalia AJA, Khan FA, Lal P, Lee S, Lu DAM;
 PI Lu Y, Patterson C, Ramkumar J, Ring HZ, Sanjarwala MS, Tang YT;
 PI Thangavelu K, Thornton M, Tribouley CM, Walla NK, Warren BA, Yang J;
 PI Yao MG, Yue H;
 XX WPI; 2002-206331/26.
 XX N-PSDB; AAD33489.
 XX New human drug metabolizing enzyme polypeptide and polynucleotide useful
 PT for diagnosing, treating and preventing cell proliferative,
 PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
 PT disorders.
 XX Claim 54; Page 154-156; 179pp; English.
 XX The invention relates to an isolated human drug metabolising enzyme (DME)
 CC polypeptide or a biologically active or immunogenic fragment of DME. DME
 CC is useful for diagnosis, treatment and prevention of cell proliferative,
 CC autoimmune/inflammatory, developmental, endocrine, eye, metabolic and
 CC gastrointestinal disorders including live disorders. Autoimmune/
 CC inflammatory disorders include acquired immunodeficiency syndrome (AIDS),
 CC adult respiratory distress syndrome, Addison's disease, atherosclerosis,
 CC allergies, anaemia, asthma, autoimmune haemolytic anaemia, autoimmune
 CC thyroiditis, Crohn's disease, atopic dermatitis, diabetes mellitus,
 CC glomerulonephritis, rheumatoid arthritis, systemic lupus erythematosus,
 CC ulcerative colitis, uveitis, viral, bacterial, protozoal, parasitic,
 CC fungal, helminthic infections and trauma. Cell proliferative disorders
 CC include cancer, arteriosclerosis, cirrhosis and psoriasis; developmental
 CC disorders include epilepsy and cataract; and endocrine disorders include
 CC disorders of hypothalamus/pituitary, disorders associated with
 CC hypopituitarism, including diabetes insipidus, hypogonadism, disorders
 CC associated with hypothyroidism including goitre, Grave's disease,
 CC pancreatic disorders such as diabetes mellitus, disorders associated with
 CC adrenals, disorders associated with gonadal steroid hormones such as
 CC endometriosis, infertility, hypergonadal disorders and gynaecomastia.
 CC Disorders of the eye include conjunctivitis and macular degeneration and
 CC metabolic disorders include diabetes, cystic fibrosis, obesity and
 CC hypocalcaemia. Gastrointestinal disorders include gastritis, peptic
 CC ulcer, hepatitis, constipation, diarrhoea, jaundice, Wilson's disease,
 CC thrombosis and hepatic tumours. DME gene is useful in gene therapy. The
 CC present sequence is human DME-10 protein
 XX Sequence 584 AA;

Query Match 100.0%; Score 3112; DB 5; Length 584;
 Best Local Similarity 100.0%; Pred. No. 1.9e-286;
 Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTVLPSTVLPSSLPTAGAGSMRWILCWSLTCLMAQTALGALHTKRPQVTKYGLQ 60

Db 1 MPSTVLPSTVLPSSLPTAGAGSMRWILCWSLTCLMAQTALGALHTKRPQVTKYGLQ 60
 QY 61 GKQMHVGKTPQVFLGVFPSPRPPIGLRFAPEPPEPKGIRDATTYPPGCLQESWGGLA 120
 Db 61 GKQMHVGKTPQVFLGVFPSPRPPIGLRFAPEPPEPKGIRDATTYPPGCLQESWGGLA 120
 QY 121 SMYVSTRERYKWLRFSEDCLYLVNYVAPARAPODGPOLPVMMVFPFGAFVGAASSYEGSDL 180
 Db 121 SMYVSTRERYKWLRFSEDCLYLVNYVAPARAPODGPOLPVMMVFPFGAFVGAASSYEGSDL 180
 QY 181 AAREKVLVFLQHLRIGIFGLSTDDSHARGNWGLLDQMAALRWVOENIAAFGGDPGNVTL 240
 Db 181 AAREKVLVFLQHLRIGIFGLSTDDSHARGNWGLLDQMAALRWVOENIAAFGGDPGNVTL 240
 QY 241 FQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLACGNHS 300
 Db 241 FQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLACGNHS 300
 QY 301 TQILVNCRLRALSGLTKMVRVSNKORFLQNFORDPEEIIWSMSPVVDGVVIPPDDPLVLTQ 360
 Db 301 TQILVNCRLRALSGLTKMVRVSNKORFLQNFORDPEEIIWSMSPVVDGVVIPPDDPLVLTQ 360
 QY 361 GKVSVPVLLGVNNLEFNNLLPYINKFPLNRQAMEKETITKWLASTRTLLNITKEOVPLV 420
 Db 361 GKVSVPVLLGVNNLEFNNLLPYINKFPLNRQAMEKETITKWLASTRTLLNITKEOVPLV 420
 QY 421 VEEYLDNVNEHDKWLRNRMDIVQDATFVYATLQTAHYHRDAGLPVLYEFEEHARGII 480
 Db 421 VEEYLDNVNEHDKWLRNRMDIVQDATFVYATLQTAHYHRDAGLPVLYEFEEHARGII 480
 QY 481 VKPRTDGADHGDEMFLFGGPPATGLSMGKEKALSQMKYWANFARTGNPDNGLPCWP 540
 Db 481 VKPRTDGADHGDEMFLFGGPPATGLSMGKEKALSQMKYWANFARTGNPDNGLPCWP 540
 QY 541 RYNKDEKYLQDLDTTRVGMKLEKKVAFWMSLYQSQRPEKQRF 584
 Db 541 RYNKDEKYLQDLDTTRVGMKLEKKVAFWMSLYQSQRPEKQRF 584
 RESULT 3
 ABG10635
 ID ABG10635 standard; protein; 509 AA.
 XX AC ABG10635;
 DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #10626.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 WPI; 2001-639362/73.
 N-PSDB; AAS74822.
 New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 40994; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ASG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 509 AA;

Query Match 76.8%; Score 2391.5; DB 4; Length 509;

Best Local Similarity 90.9%; Pred. No. 5e-218; Indels 31; Gaps 3;
Matches 461; Conservative 2; Mismatches 13;

QY 109 PG---CLQESWGQASMTVSTRERYKMLRFSEDCLYLVNVPAPAPAGDPOLPVMWPPGG 165
Db 3 FGARCLHEFWGQASMTVSTRERYKMLRFNEDCLYLVNVPAPAPAGDPOLPVMWPPGG 62
QY 166 AFIVGAASSYGGSLAAREKVLVLOHRLGIFGLTSDSHARGNGLDQMAALRWVQ 225
Db 63 AFIVGAASSYGGSLAAREKVLVLOHRLGIFGLTSDSHARGNGLDQMAALRWVQ 122
QY 226 ENIAAFGDPQCNV-TLFGQSAGANSISGLMWSPLASGLFHRAISQSGTALFRIFITSNPL 284
Db 123 ENIAAFGRPREIITLFGQSAGANSISGLMWSPLASGLFHRAISQSGTALFRIFITSNPL 182
QY 285 KVAKKVAHLACGNHNSQTILVNCILRALSGTKVMRVSNKMRFLQINFORDEEIIWMSVPV 344
Db 183 KVAKKVAHLACGNHNSQTILVNCILRALTRAKVMRVSNKMRFLQINFORDEEIIWMSVPV 242
QY 345 VDGVIIPDDPLVLTQGVSSVPVLLGVNLEFNWLLPYTMKPLNRAQVRKETTITKMLW 404
Db 243 VDGVIIPDDPLVLTQGVSSVPVLLGVNLEFNWLLPYTMKPLNRAQVRKETTITKMLW 302
QY 405 STRILL-----NITKEQVPLVVEEYLDNVNNEHDKMLR 437
Db 303 STRILLAKNSGABHGSKSLVGPPLAQLAPRPNITKEQVPLVVEEYLDNVNNEHDKMLR 362
QY 438 NRMVDIVODATFVYATQTAHYHHDAGLVPVLYFEFHARGIIVKPTDGDHGDWYFL 497
Db 363 NRMVDIVODATFVYATQTAHYHHDAGLVPVLYFEFHARGIIVKPTDGDHGDWYFL 422
QY 498 FGGPFATGSLMGKALKSLQWKYKWFANFARTGNPDNGLPCWPRYNKDEKYLQLDITTRV 557
Db 423 FGGPFATGSLMGKALKSLQWKYKWFANFARTGNPDNGLPCWPRYNKDEKYLQLDITTRV 482
QY 558 GKKLKEKQAFWMSLYGQSRPEKQRF 584
Db 483 GKKLKEKQAFWMSLYGQSRPEKQRF 509

RESULT 4

RAY41723

ID RAY41723 standard; protein; 545 AA.

XX AC RAY41723;
XX DT 07-DEC-1999 (first entry)
XX DE Human PRO873 protein sequence.
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX KW secreted protein; transmembrane protein.
XX OS Homo sapiens.
XX PN WO9946281-A2.
XX PD 16-SEP-1999.
XX PF 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1998; 98US-0077450P.
XX PR 11-MAR-1998; 98US-0077632P.
XX PR 11-MAR-1998; 98US-0077641P.
XX PR 11-MAR-1998; 98US-0077649P.
XX PR 12-MAR-1998; 98US-0077791P.
XX PR 13-MAR-1998; 98US-0078004P.
XX PR 17-MAR-1998; 98US-00040220.
XX PR 20-MAR-1998; 98US-0078886P.
XX PR 20-MAR-1998; 98US-0078910P.
XX PR 20-MAR-1998; 98US-0078936P.
XX PR 20-MAR-1998; 98US-0078939P.
XX PR 25-MAR-1998; 98US-0079294P.
XX PR 26-MAR-1998; 98US-0079565P.
XX PR 27-MAR-1998; 98US-0079663P.
XX PR 27-MAR-1998; 98US-0079664P.
XX PR 27-MAR-1998; 98US-0079689P.
XX PR 27-MAR-1998; 98US-0079728P.
XX PR 27-MAR-1998; 98US-0079786P.
XX PR 30-MAR-1998; 98US-0079920P.
XX PR 30-MAR-1998; 98US-0079923P.
XX PR 31-MAR-1998; 98US-0080105P.
XX PR 31-MAR-1998; 98US-0080107P.
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XX PR 31-MAR-1998; 98US-0080194P.
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XX PR 01-APR-1998; 98US-0080333P.
XX PR 01-APR-1998; 98US-0080334P.
XX PR 08-APR-1998; 98US-0081049P.
XX PR 08-APR-1998; 98US-0081070P.
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XX PR 09-APR-1998; 98US-0081195P.
XX PR 09-APR-1998; 98US-0081203P.
XX PR 09-APR-1998; 98US-0081229P.
XX PR 15-APR-1998; 98US-0081817P.
XX PR 15-APR-1998; 98US-0081838P.
XX PR 15-APR-1998; 98US-0081952P.
XX PR 15-APR-1998; 98US-0081955P.
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XX PR 22-APR-1998; 98US-0082700P.
XX PR 22-APR-1998; 98US-0082704P.
XX PR 23-APR-1998; 98US-0082804P.
XX PR 23-APR-1998; 98US-0082767P.
XX PR 27-APR-1998; 98US-0082796P.
XX PR 28-APR-1998; 98US-0083336P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 29-APR-1998; 98US-0083392P.
XX PR 29-APR-1998; 98US-0083495P.
XX PR 29-APR-1998; 98US-0083496P.
XX PR 29-APR-1998; 98US-0083499P.
XX PR 29-APR-1998; 98US-0083500P.
XX PR 29-APR-1998; 98US-0083545P.
XX PR 29-APR-1998; 98US-0083554P.

PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00844848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-602746/68.
 DR N-PSDB; AAS45953.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 11; Fig 58; 774pp; English.
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX SQ Sequence 545 AA;
 Query Match 65.1%; Score 2026.5; DB 4; Length 545;
 Best Local Similarity 80.3%; Pred. No. 2.8e-183;
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;
 QY 6 LPSTVLPSSLPTAGAGWNRWILCNSLTCLMAQTALGALHTKRPQVTKYTLQKQMH 65
 DB 47 LGSTSTPAITSAPSSGFGTGLFGSKPATGTLGGTNTGALHTKRPQVTKYTLQKQMH 106
 QY 66 VGKTPIQVFLGVPSRPPGLIRFAPPEPPKWKIRDTATYPDG----- 110
 DB 107 VGKTPIQVFLGVPSRPPGLIRFAPPEPPKWKIRDTATYPDGNSALSPGNSAVARS 166
 QY 111 -----CLOESWQQLASMYSTRERYKWLRFSEDCILYLVNY 145
 DB 167 RLATASRVSQASLLPQLPSVWNGYRCLQESWQQLASMYSTRERYKWLRFSEDCILYLVNY 226
 QY 146 APARAPDPPQPMWTFPGGATVGAASSYEGSDLAAREKVVFLQHLRIGFGLSTDD 205
 DB 227 APARAPDPPQPMWTFPGGATVGAASSYEGSDLAAREKVVFLQHLRIGFGLSTDD 286
 QY 206 SHARGNWGLLDQVAALRWVQENIAAFGGDPGNVTILFGSAGAMSTISGLMSPGLASGLPHR 265

DB 287 SHARGNWGLLDQVAALRWVQENIAAFGGDPGNVTILFGSAGAMSTISGLMSPGLASGLPHR 346
 QY 266 AISOQGTALFLPITSNPLKVAKKVAHLACGNHNSSTQILVNCRLALSGTKVMRYSNKMR 325
 DB 347 AISOQGTALFLPITSNPLKVAKKVAHLACGNHNSSTQILVNCRLALSGTKVMRYSNKMR 406
 QY 326 LQLNFRQDPPEEIIWMSMSPVWGVIPDDPLVLLTGQKVSSVPYLLGVNNEFNWLLPYIM 385
 DB 407 LQLNFRQDPPEEIIWMSMSPVWGVIPDDPLVLLTGQKVSSVPYLLGVNNEFNWLLPY-- 464
 QY 386 KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNNEHDMKMLRNRMMDIVQ 445
 DB 465 -----NITKEQVPLVVEEYLDNNEHDMKMLRNRMMDIVQ 499
 QY 446 DATFVYATLQTAHYRD 462
 DB 500 DATFVYATLQTAHYRE 516

RESULT 6

ABUS8428

ID ABUS8428 standard; protein; 545 AA.

XX AC ABUS8428;

XX DT 15-APR-2003 (first entry)

XX DE Human PRO polypeptide #29.

XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;

XX KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;

XX KW antibody-dependent enzyme mediated prodrug therapy.

XX OS Homo sapiens.

XX PN US2003027272-A1.

XX PD 06-FEB-2003.

XX PF 21-JUN-2002; 2002US-00176492.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 17-OCT-1997; 97US-0062350P.

XX PR 21-OCT-1997; 97US-0063486P.

XX PR 24-OCT-1997; 97US-0063420P.

XX PR 28-OCT-1997; 97US-0063121P.

XX PR 28-OCT-1997; 97US-0063540P.

XX PR 28-OCT-1997; 97US-0063541P.

XX PR 28-OCT-1997; 97US-0063564P.

XX PR 29-OCT-1997; 97US-0063734P.

XX PR 31-OCT-1997; 97US-0063870P.

XX PR 31-OCT-1997; 97US-0064103P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 21-NOV-1997; 97US-0066120P.

XX PR 24-NOV-1997; 97US-0066466P.

XX PR 24-NOV-1997; 97US-0066772P.

XX PR 11-DEC-1997; 97US-0069335P.

XX PR 12-DEC-1997; 97US-0069425P.

XX PR 17-DEC-1997; 97US-0069870P.

XX PR 18-DEC-1997; 97US-0068017P.

XX PR 10-MAR-1998; 98US-0077450P.

XX PR 11-MAR-1998; 98US-0077632P.

XX PR 20-MAR-1998; 98US-0077649P.

XX PR 20-MAR-1998; 98US-0078866P.

XX PR 20-MAR-1998; 98US-0078939P.

XX PR 27-MAR-1998; 98US-0079664P.

XX PR 27-MAR-1998; 98US-0079786P.

XX PR 31-MAR-1998; 98US-0080107P.

XX PR 31-MAR-1998; 98US-0080194P.

XX PR 01-APR-1998; 98US-0080327P.


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PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
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PR 17-JUN-1998; 98US-0089338P.
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PR 02-SEP-1998; 98US-0098803P.
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PR 09-SEP-1998; 98US-0098602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
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PR 15-SEP-1998; 98US-0100388P.
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PR 16-SEP-1998; 98US-0101751P.

PR 16-SEP-1998; 98WO-US019330.
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PR 23-SEP-1998; 98US-0101471P.
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PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
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PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.

Query Match 65.1%; Score 2026.5; DB 6; Length 545;
Best Local Similarity 80.3%; Pred. No. 2.8e-183;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY 6 LPSTVLPSELLPTAGAGNSRWILWSLTLCLMAQTALCALHTKRPQVTKYGTLOGKQMH 65
Db 47 LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGCTINTGALHTKRPQVTKYGTLOGKQMH 106
QY 66 VGKTIQVFLGVFPRPPLGLIRPAPPPEPPPKWGIKIRDAITYPG- 110
Db 107 VGKTIQVFLGVFPRPPLGLIRPAPPPEPPPKWGIKIRDAITYPGWSLALSPGWSAVARS 166
QY 111 -----CLOESWGQLASMTVSTRERYKWLRFSEDCILYNVY 145
Db 167 RLUTATSASRVQASLLPQLPSVWGVYRCLOESWGQLASMTVSTRERYKWLRFSEDCILYNVY 226
QY 146 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLFQHRIGIFGLSTDD 205
Db 227 APARAPGDPQLPVMVWFPGGAFIVGAASSYEGSDLAAREKVVLFQHRIGIFGLSTDD 286
QY 206 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSTISGLMWSPLASGLFHR 265
Db 287 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSTISGLMWSPLASGLFHR 346
QY 266 AISQSGTALFRLFITSNPLKVAKKVAHLACGNHNSTOILVNCRLALSGLTKMVRVSNKMRF 325
Db 347 AISQSGTALFRLFITSNPLKVAKKVAHLACGNHNSTOILVNCRLALSGLTKMVRVSNKMRF 406
QY 326 LQINFORDEEIIWMSPPWDGWIPIDDPLVLLTQGVSSVFPYLLGVNLEFNWLLPYIM 385
Db 407 LQINFORDEEIIWMSPPWDGWIPIDDPLVLLTQGVSSVFPYLLGVNLEFNWLLPY-- 464
QY 386 KPFLNRQAMRKETITKMLWSTLTILNITKEQVPLVVEYLDNVNHEHDKMLNRMDIVQ 445
Db 465 -----NITKEQVPLVVEYLDNVNHEHDKMLNRMDIVQ 499
QY 446 DATEFVYATLQTAHYHRD 462
Db 500 DATEFVYATLQTAHYHRE 516

RESULT 8
ABU84291
ID ABU84291 standard; protein; 545 AA.
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PR	18-AUG-1998;	98US-0096949P.	Query Match	65.1%;	Score 2026.5;	DB 6;	Length 545;
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PR	18-AUG-1998;	98US-0097022P.	Matches 399;	Conservative	5;	Mismatches 26;	Indels 67;
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PR	26-AUG-1998;	98US-0097971P.					
PR	26-AUG-1998;	98US-0097974P.					
PR	26-AUG-1998;	98US-0098014P.					
PR	01-SEP-1998;	98US-0098716P.					
PR	01-SEP-1998;	98US-0098723P.					
PR	02-SEP-1998;	98US-0098803P.					
PR	02-SEP-1998;	98US-0098821P.					
PR	02-SEP-1998;	98US-0098843P.					
PR	09-SEP-1998;	98US-0099602P.					
PR	10-SEP-1998;	98US-0099741P.					
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PR	10-SEP-1998;	98US-0099812P.					
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PR	16-SEP-1998;	98US-0100662P.					
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PR	23-SEP-1998;	98US-0101472P.					
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PR	24-SEP-1998;	98US-0101738P.					
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PR	24-SEP-1998;	98US-0101922P.					
PR	25-SEP-1998;	98US-0101786P.					
PR	29-SEP-1998;	98US-0102207P.					
PR	29-SEP-1998;	98US-0102240P.					
PR	29-SEP-1998;	98US-0102330P.					
PR	29-SEP-1998;	98US-0102331P.					
PR	30-SEP-1998;	98US-0102487P.					
PR	30-SEP-1998;	98US-0102570P.					
PR	30-SEP-1998;	98US-0102571P.					
PR	01-OCT-1998;	98US-0102684P.					
PR	01-OCT-1998;	98US-0102687P.					
PR	02-OCT-1998;	98US-0102965P.					
PR	06-OCT-1998;	98US-0103258P.					
PR	06-OCT-1998;	98US-0103449P.					
PR	07-OCT-1998;	98US-00168978.					

Query Match 65.1%; Score 2026.5; DB 6; Length 545;

Best Local Similarity 80.3%; Pred. No. 2.8e-183;

Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY	6	LPSTVLSPLTPAGAGMSRWILCWSLTLCIMAOALCALHTKRPQVWTKYGLQKQMH	65
DB	47	LGSTSTPATTAPSSGGTGLFGSKPATGFTLGGTNGALHTKRPQVWTKYGLQKQMH	106
QY	66	VGKTPIQVFLGVFFSRPPLGLIRFAPPEPPFPWKGRDATTYPG-----	110
DB	107	VGKTPIQVFLGVFFSRPPLGLIRFAPPEPPFPWKGRDATTYPGWSIALSPGWSAVARS	166
QY	111	-----CLOESGOLASMYVSTRERYKMLRFSEDCLYLNXY	145
DB	167	RLTATSASRVQASLLPQLSVNGVRCLOESGOLASMYVSTRERYKMLRFSEDCLYLNXY	226
QY	146	APARAPGPQPLPVMVWFFGGAFIVGAASSYEGSDLAAREKVVLPVFLQHLGIFGFLSTDD	205
DB	227	APARAPGPQPLPVMVWFFGGAFIVGAASSYEGSDLAAREKVVLPVFLQHLGIFGFLSTDD	286

QY	206	SHARGNWLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR	265
DB	287	SHAFGNWGLLDQMAALEWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR	346
QY	266	AISQSGTALFRLFTITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGLTKVMRYSNRQRF	325
DB	347	AISQSGTALFRLFTITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGLTKVMRYSNRQRF	406
QY	326	LQNFQRPDPBEIIWMSFPVVDGVIPDDPLVLLTQGVKSSVPYLLGVNNLEFNWLLPYIM	385
DB	407	LQNFQRPDPBEIIWMSFPVVDGVIPDDPLVLLTQGVKSSVPYLLGVNNLEFNWLLPY--	464
QY	386	KFPLNRQAMRKETITKMLWSTRLNITKEQVPLVVEEYLDNVNNEHDKMLRNRMDIVQ	445
DB	465	-----NITKEQVPLVVEEYLDNVNNEHDKMLRNRMDIVQ	499
QY	446	DATFVYATLQTAHYHRD	462
DB	500	DATFVYATLQTAHYHRE	516
RESULT 9			
ABR66165			
ID	ABR66165 standard; protein; 545 AA.		
XX	AC ABR66165;		
XX	DT 05-AUG-2003 (first entry)		
DE	Human secreted polypeptide PRO873, SEQ ID NO:58.		
KW	Human; PRO; secreted protein; transmembrane protein;		
KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		
KW	liver; drug screening; transgenic animal; genetic analysis;		
KW	antiarthritic; vulnery; gene therapy.		
OS	Homo sapiens.		
XX	US2003027278-A1.		
XX	06-FEB-2003.		
XX	21-JUN-2002; 2002US-00176987.		
PR	18-SEP-1997;	97US-0059263P.	
PR	18-SEP-1997;	97US-0059268P.	
PR	17-OCT-1997;	97US-0064250P.	
PR	21-OCT-1997;	97US-0063486P.	
PR	24-OCT-1997;	97US-0063120P.	
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PR	28-OCT-1997;	97US-0063540P.	
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PR	18-DEC-1997;	97US-0068017P.	
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PR	11-MAR-1998;	98US-0077632P.	
PR	11-MAR-1998;	98US-0077649P.	
PR	20-MAR-1998;	98US-0078866P.	

PR 20-MAR-1998; 98US-0078933P.
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PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
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PR 18-SEP-1998; 98US-0100849P.
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PR	01-OCT-1998;	98US-0102687P.	
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Matches 399; Conservative			5; Mismatches 26; Indels 67; Gaps 2;
QY	6	LPSTVPSLLPTAGAGSMRWILCWSLTLCLMAQALGALHTKRPQVVTKYGTLOGKQWH	65
DB	47	LGSTSTPATTSAPSSGFGTLGSKPATGTTLGNTGALHTKRPQVVTKYGTLOGKQWH	106
QY	66	VGKTPIQVLGVFPSPPLGILRPAPPEPPEPWKGRDATTTPPG-----	110
DB	107	VGKTPIQVLGVFPSPPLGILRPAPPEPPEPWKGRDATTTPPGWSLSPQWSAVARS	166
QY	111	-----CLOESWGOLASMYSTRERYKWLRFSEDCLYLVNY	145
DB	167	RLTATGASRVOAGLLPQPLSVWGRCLOESWGOLASMYSTRERYKWLRFSEDCLYLVNY	226
QY	146	APARAPGDPQLPVWVFPFGGAFIVGAASSYEGSDLAAREKVVLFVLOHRLGIFGFLSTDD	205
DB	227	APARAPGDPQLPVWVFPFGGAFIVGAASSYEGSDLAAREKVVLFVLOHRLGIFGFLSTDD	286
QY	206	SHARGNWLLDDQAAALRWVOENIAAEGDPGNVTLFGQSAGAMISGLMWSPPLASGLFHR	265
DB	287	SHARGNWLLDDQAAALRWVOENIAAEGDPGNVTLFGQSAGAMISGLMWSPPLASGLFHR	346
QY	266	AISQSGTALFRLFTTSNPLKVAKVAKVLAHCNHNSTQILVNCRLALSGTKVMSVSKMRF	325
DB	347	AISQSGTALFRLFTTSNPLKVAKVAKVLAHCNHNSTQILVNCRLALSGTKVMSVSKMRF	406
QY	326	LQNFORDPBEIIMSPPVGVVIPPDPVLVLTQGVKSSVPYLLGWNLEFNWLLPYIM	385
DB	407	LQNFORDPBEIIMSPPVGVVIPPDPVLVLTQGVKSSVPYLLGWNLEFNWLLPY--	464
QY	386	KFPLNRQAMRKETITKMLWSTRLNITKEQVPLVVEEYLDNVNEDWKLNRNMDIVQ	445
DB	465	-----NITKEQVPLVVEEYLDNVNEDWKLNRNMDIVQ	499
QY	446	DATEVYATLQTAHYHRD	462
DB	500	DATEVYATLQTAHYHRE	516
RESULT 10			
ID	ABR65555	standard; protein; 545 AA.	
AC	ABR65555;		
XX	ABR65555;		
DT	05-AUG-2003	(first entry)	
DE	Human secreted polypeptide PRO873, SEQ ID NO:58.		
KW	Human; PRO; secreted protein; transmembrane protein;		
KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		
KW	liver; drug screening; transgenic animal; genetic analysis;		
KW	antiarthritic; vulnery; gene therapy.		
OS	Homo sapiens.		
XX	US2003036159-A1.		
PD	20-FEB-2003.		
XX	02-JUL-2002; 2002US-00188773.		

PR	18-SEP-1997;	97US-0059263P.	
PR	18-SEP-1997;	97US-0059366P.	
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PR 10-SEP-1998;	98US-0099602P.		
PR 10-SEP-1998;	98US-0099741P.		
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Query Match 65.1%; Score 2026.5; DB 6; Length 545;

Best Local Similarity 80.3%; Pred. No. 2.8e-183;

Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY	6	LPSTVLPSLPTAGAGWMSRWILCWSLTLCLMAQTALGALHTKRPQVWTKYGTLOGKQH	65
DB	47	LGSTSTATTSSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVWTKYGTLOGKQH	106
QY	66	VKTPIQVFLGVPSRPPGLILFAPPEPPKWKIRDAATYPG-----	110
DB	107	VKTPIQVFLGVPSRPPGLILFAPPEPPKWKIRDAATYPGWSLSPGSAVARS	166
QY	111	-----CLQESWGOLASMYSTRERYKWLRFSEDCILNVY	145
DB	167	RLTATSASRVQASLLPQLSVWGYRCLQESWGOLASMYSTRERYKWLRFSEDCILNVY	226
QY	146	APAPAGDPQPVWMPFGGAFIVGAASSYEGSDLAAREKVLVFLQHLGIFGFLSTDD	205
DB	227	APAPAGDPQPVWMPFGGAFIVGAASSYEGSDLAAREKVLVFLQHLGIFGFLSTDD	286
QY	206	SHARGNGLLDQAAALRWQENIAAEGDPNTVLFGQSAGANSISGLMKSPGLFHR	265
DB	287	SHARGNGLLDQAAALRWQENIAAEGDPNTVLFGQSAGANSISGLMKSPGLFHR	346
QY	266	AISQSGTALFRLFITSNPLKVAKKVAHLACGNHNSITQILVNCRLALSGLTKWVSNNKMF	325
DB	347	AISQSGTALFRLFITSNPLKVAKKVAHLACGNHNSITQILVNCRLALSGLTKWVSNNKMF	406
QY	326	LQNFQDPDEIITWSMSPVVDGVIIPDDPLVLTQKVSVPYLLGVNNLEFNLLPYM	385
DB	407	LQNFQDPDEIITWSMSPVVDGVIIPDDPLVLTQKVSVPYLLGVNNLEFNLLPYM	464
QY	386	KFPLNQAMRKETITKMLMSTRLLNITKEQVPLVVEEYLDNVNHDWMLNRMMDIVQ	445
DB	465	-----NITKEQVPLVVEEYLDNVNHDWMLNRMMDIVQ	499
QY	446	DATFVATLQTAHYHRD	462
DB	500	DATFVATLQTAHYHRE	516

RESULT 11

ABU99495
ID AEU99495 standard; protein; 545 AA.
XX AC ABU99495;
XX 09-AUG-2003 (first entry)
DT DE Human secreted/transmembrane protein (PRO) #29.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX OS Homo sapiens.
XX PN US2003040070-A1.
XX PD 27-FEB-2003.
XX PF 27-JUN-2002; 2002US-00184627.
XX PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 11-DEC-1997; 97US-0066772P.
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PR	10-SEP-1998;	98US-0098743P;
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PR	10-SEP-1998;	98US-0098763P;
PR	10-SEP-1998;	98US-0098812P;
PR	15-SEP-1998;	98US-0100632P;
PR	16-SEP-1998;	98US-0100662P;

RESULT 14
ID ABR68104 standard; protein; 545 AA.
XX
AC ABR68104;
DT 11-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO873, SEQ ID NO:58.
XX
KW Human; PRC; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027264-A1.
PD 06-FEB-2003.
XX
XX 18-JUN-2002; 2002US-00174579.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059263P.
PR 17-OCT-1997; 97US-0022250P.
PR 21-OCT-1997; 97US-0063486P.
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PR 24-OCT-1997; 97US-0063121P.
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PR 28-OCT-1997; 97US-0063541P.
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PR 31-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0064103P.
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PR 21-NOV-1997; 97US-0065120P.
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PR 24-JUL-1998; 98US-0094006P.

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PR	26-AUG-1998;	98US-0098014P.	
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PR	10-SEP-1998;	98US-0099812P.	
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PR	16-SEP-1998;	98US-0101751P.	
PR	16-SEP-1998;	98US-0101933P.	
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PR	17-SEP-1998;	98US-0100930P.	
PR	18-SEP-1998;	98US-0100849P.	
PR	18-SEP-1998;	98US-0101014P.	
PR	18-SEP-1998;	98US-0101068P.	
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PR	24-SEP-1998;	98US-0101743P.	
PR	24-SEP-1998;	98US-0101922P.	
PR	25-SEP-1998;	98US-0101786P.	
PR	29-SEP-1998;	98US-0102207P.	
PR	29-SEP-1998;	98US-0102240P.	
PR	29-SEP-1998;	98US-0102330P.	
PR	29-SEP-1998;	98US-0102331P.	
PR	30-SEP-1998;	98US-0102487P.	
PR	30-SEP-1998;	98US-0102570P.	
PR	30-SEP-1998;	98US-0102571P.	
PR	01-OCT-1998;	98US-0102664P.	
PR	01-OCT-1998;	98US-0102687P.	
Query Match			65.1%; Score 2026.5; DB 6; Length 545;
Best Local Similarity			80.3%; Pred. No. 2.8e-183;
Matches 399; Conservative			5; Mismatches 26; Indels 67; Gaps 2;
QY	6	LPSTVLPBLLTAGAGSMRWILCNSLTCLMAOTALGALHTKEPOVVTYGTILQKQMH	65
DB	47	LGSTSTPATTAPSGSGFTGFGSKPATGFTLGNTGALHTKRPQVVTYGTILQKQMH	106
QY	66	VGKTPIQVFLGVPSRPLGIRFAPPEPPFPWKGIRDATTYPG-----	110
DB	107	VGKTPIQVFLGVPSRPLGIRFAPPEPPFPWKGIRDATTYPGWSLALSPGWSAVARS	166
QY	111	-----CLOESGOLASMYVSTRERYKWLRFSEDCILYLVY	145
DB	167	RLTATSASRVOASLLPQLPSVWGYRCLOESGOLASMYVSTRERYKWLRFSEDCILYLVY	226

QY	146	APARAPGDPOLPYVMWPPGAFIVGAASSYEGSDLAAREKVVLFVFLQHRIGIFGFLSTDD	205
DB	227	APARAPGDPOLPYVMWPPGAFIVGAASSYEGSDLAAREKVVLFVFLQHRIGIFGFLSTDD	286
QY	206	SHAEGNWGLLDQMAALRWQENIAAFGGDPGNVTLFQOSAGAMSIISGLMWSPLASGLFHR	265
DB	287	SHAEGNWGLLDQMAALRWQENIAAFGGDPGNVTLFQOSAGAMSIISGLMWSPLASGLFHR	346
QY	266	AISOSGTALFRLFTTSNPLKVAKVAHLACNHNSTOILVNCRLRSLSGTKVMRVSNKQRF	325
DB	347	AISOSGTALFRLFTTSNPLKVAKVAHLACNHNSTOILVNCRLRSLSGTKVMRVSNKQRF	406
QY	326	LQINFQRPDEEIIWSMSPVVDGVIPDDPLVLTQGVKSVVYLLGVNNLEFNWLLPYIM	385
DB	407	LQINFQRPDEEIIWSMSPVVDGVIPDDPLVLTQGVKSVVYLLGVNNLEFNWLLPY--	464
QY	386	KFPLNRQAMRKETITKMLWSTRTLLNITKQVPLWVEEYLDNVNEHDWKMLRNMMDIVQ	445
DB	465	-----NITKQVPLWVEEYLDNVNEHDWKMLRNMMDIVQ	499
QY	446	DATFVYATLQTAHYHRD	462
DB	500	DATFVYATLQTAHYHRE	516
RESULT 15			
ABU96157			
ID	ABU96157 standard; protein; 545 AA.		
XX	AC ABU96157;		
XX	AC ABU96157;		
DT	25-JUL-2003 (first entry)		
DE	Novel human secreted and transmembrane protein PRO873.		
XX	Human; secreted and transmembrane protein; PRO; transgenic animal;		
KW	knockout; chromosome identification; tissue typing; tumour;		
KW	chondrocyte proliferation; chondrocyte differentiation;		
KW	tumor necrosis factor-alpha release stimulator.		
OS	Homo sapiens.		
XX	US20030306144-A1.		
PN	20-FEB-2003.		
PD	01-JUL-2002; 2002US-00187601.		
PF	18-SEP-1997; 97US-0059263P.		
XX	18-SEP-1997; 97US-0059266P.		
PR	17-OCT-1997; 97US-0062250P.		
PR	21-OCT-1997; 97US-0063486P.		
PR	24-OCT-1997; 97US-0063120P.		
PR	24-OCT-1997; 97US-0063121P.		
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PR	28-OCT-1997; 97US-0063541P.		
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PR	28-OCT-1997; 97US-0063564P.		
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PR	31-OCT-1997; 97US-0063870P.		
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PR	13-NOV-1997; 97US-0065311P.		
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PR	24-NOV-1997; 97US-0066466P.		
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PR	30-SEP-1998;	98US-0102571P.	
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Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;			
Qy	6	LPSTVLPSLLPTAGAGMSRWILCWSLTLCLMAQTALGALHTKRPQVTKYGTLOGKQMH	65
Db	47	LGSTSTPATTSAPSSGFCGLFSKPKATGFTLGSTNTGALHTKRPQVTKYGTLOGKQMH	106
Qy	66	VGKTPIQVFLGVFSPRPPLGILRFAPPEPEPWKGIKRDATTYPPG-----	110
Db	107	VGKTPIQVFLGVFSPRPPLGILRFAPPEPEPWKGIKRDATTYPPGWSLALSPGWSAVARS	166
Qy	111	-----CLOESWGOLASMYSTREYKWLRFSEDCLYLNVY	145
Db	167	RLTATSASRVQASLLPOPLSVWGYRCLQESWGOLASMYSTREYKWLRFSEDCLYLNVY	226
Qy	146	APARAPGDPQLPVNWFPPGGAFIVGAASSYEGSDLAAREKVLVFLQHLRGLGIFGLSTDD	205
Db	227	APARAPGDPQLPVNWFPPGGAFIVGAASSYEGSDLAAREKVLVFLQHLRGLGIFGLSTDD	286
Qy	206	SHARGNWGLLDQMAALRWQENIAAFGGDEGNVTLFGOSAGAMSI SGLMMSPLASGLFHR	265
Db	287	SHARGNWGLLDQMAALRWQENIAAFGGDEGNVTLFGOSAGAMSI SGLMMSPLASGLFHR	346
Qy	266	AISQSGTALFRLFTITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGLTKVMRVSNKMRF	325
Db	347	AISQSGTALFRLFTITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGLTKVMRVSNKMRF	406
Qy	326	LQLNFORDPBEIIMSPPVVDGVIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM	385
Db	407	LQLNFORDPBEIIMSPPVVDGVIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY--	464
Qy	386	KFPLNRQAMRKETTITKMLWSTRLNITKEQVPLVVEEYLDNVNEHDKMLRNRMMDIVQ	445
Db	465	-----NITKEQVPLVVEEYLDNVNEHDKMLRNRMMDIVQ	499
Qy	446	DATEVYATLQTAHYHRD	462
Db	500	DATEVYATLQTAHYHRE	516

Search completed: August 3, 2004, 22:27:04
Job time : 59 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 22:26:01 ; Search time 19 Seconds
(without alignments)
1586.819 Million cell updates/sec

Title: US-10-001-227-2
Perfect score: 3112
Sequence: 1 MBSTVLPSTVLPSSLPTAGA.....KMAFMMSLYQSQRPKQRF 584

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents RA: *
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PGTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1251.5	40.2	566	3	US-09-264-737-2
2	1169.5	37.6	584	2	US-08-845-295A-2
3	1169.5	37.6	584	3	US-09-140-933-2
4	1169.5	37.6	584	3	US-09-146-661-2
5	1169.5	37.6	584	3	US-09-150-515-2
6	1145	36.8	581	4	US-10-023-315-2
7	1133	36.4	539	3	US-09-264-737-1
8	983.5	31.6	454	3	US-08-446-100-26
9	983.5	31.6	454	3	US-08-446-100-30
10	983.5	31.6	454	3	US-08-446-100-31
11	981.5	31.5	454	3	US-08-446-100-27
12	977.5	31.4	454	3	US-08-446-100-28
13	977.5	31.4	454	3	US-08-446-100-29
14	908.5	29.2	574	4	US-10-023-315-4
15	849	27.3	836	4	US-09-491-356C-21
16	831	26.7	848	4	US-09-491-356C-22
17	820.5	26.4	823	4	US-09-491-356C-23
18	788	25.3	843	4	US-09-491-356C-20
19	787.5	25.3	617	2	US-08-370-156-6
20	787.5	25.3	617	3	US-08-844-095-6
21	787	25.3	600	2	US-08-370-156-4
22	787	25.3	600	3	US-08-814-095-4
23	787	25.3	600	1	US-08-975-084-1
24	787	25.3	614	1	US-07-732-962A-2
25	787	25.3	614	2	US-08-370-156-2
26	787	25.3	614	3	US-08-446-100-19
27	787	25.3	614	3	US-08-814-095-2

28	787	25.3	614	5	FCT-US92-06106-2	Sequence 2, Appli
29	786	25.3	614	3	US-08-446-100-21	Sequence 21, Appl
30	785	25.2	614	3	US-08-446-100-20	Sequence 20, Appl
31	785	25.2	614	3	US-08-446-100-25	Sequence 25, Appl
32	785	25.2	614	3	US-08-446-100-23	Sequence 23, Appl
33	782	25.1	614	3	US-08-446-100-22	Sequence 22, Appl
34	727.5	23.4	553	4	US-09-491-356C-24	Sequence 24, Appl
35	727.5	23.4	575	1	US-08-348-920-2	Sequence 2, Appli
36	724.5	23.3	575	1	US-08-348-920-1	Sequence 1, Appli
37	722.5	23.2	606	4	US-09-347-878-34	Sequence 34, Appl
38	722	23.2	597	1	US-08-462-884A-1	Sequence 1, Appli
39	722	23.2	597	1	US-08-481-881B-1	Sequence 1, Appli
40	722	23.2	597	2	US-08-123-960-1	Sequence 1, Appli
41	717.5	23.1	605	1	US-08-462-884A-3	Sequence 3, Appli
42	717.5	23.1	605	1	US-08-461-881B-3	Sequence 3, Appli
43	717.5	23.1	605	2	US-09-123-960-3	Sequence 3, Appli
44	712.5	22.9	602	3	US-08-446-100-1	Sequence 1, Appli
45	712.5	22.9	602	3	US-08-446-100-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-264-737-2
; Sequence 2, Application US/09264737A
; Patent No. 6107549
; GENERAL INFORMATION:
; APPLICANT: Ruff, Paul C.C.
; TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
; TITLE OF INVENTION: Expression of Esterase Enzymes
; FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
; CURRENT APPLICATION NUMBER: US/09/264,737A
; CURRENT FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: 60/077,377
; EARLIER FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Rabbit
US-09-264-737-2

Query Match	40.2%	Score	1251.5	DB 3	Length	566
Best Local Similarity	43.7%	Pred. No.	2.5e-119	Indels	27	Gaps 11
Matches	248	Conservative	117	Mismatches	175	
QY	28	LCWSLTLCIMAOALGALHTKEPQVTKYGTLOQKQMHVK	-----TPIQVFLGVPP	79		
Db	7	LWV---LFLAACTANG--HPSAPPV--DTVKGVKVL--GKFSLEGEPAQVAVFLGVPP	56			
QY	80	SRPPIGLIRFAPPEPPEPWKGIARDATTYPGCLQE--SWGQLASMYVSTRERYKWLRFSE	137			
Db	57	AKPPLGLSLRFAPQPQAESNSHVKNNTSYPPMCSQDAVSHMLSELFTRKNENIP-LKFSE	115			
QY	138	DCLYLNVPAPAPGDPOLPVMMVFPFGAFIVGAASSEGSGLAAREKVVLFVQLRLGI	197			
Db	116	DCLYLNITPDLTKRGLPVMVWINGGLWGGASTYDGLALSAHENVVVTIQVRLGI	175			
QY	198	FGFLSTDDSHAGNKGLLDQMAALRWQENIAFGDQGNVTLFQCSAGAMISGLMMSP	257			
Db	176	WGFFSTGDESHSGNKGHLDOVRALRWQDNIAFGGDFGSVTFIFGESAGQSVSTILLSP	235			
QY	258	LASGLFPHRAISGGTALFELTTSNPLKVAKVHLAGCNHNSTOILVNCRLALSGTKVM	317			
Db	236	LTKNFHRAISSEGVALLSSLPFRKNTKSLAEKIAIEAGCKTTTSAMVHCLRQKTEBELM	295			
QY	318	RYSNKMRFQLQNFQRPDEEIIWMSGFVVDGVVIPPDLVLLTQGVSSVPVLLGVNNEF	377			
Db	296	EVTLKMKFWALDVGDPKENTAFLTVIDGVLLKPAPAEILAEKKYNMLPYMVGINQOBF	355			

QY 378 NWLLP-YIMKPLNQRQMKETITKMLNSTLNLITKEQVPLVVEEYLDNNEHDKML 436
 DB 356 GWIPQMLGVLSEGLDKQATLWKSYPVNVSKELTPVATEKYLGGTDDPVKK-- 413
 QY 437 RNRMMDIVQDATFVYATLQTAHYHRDAGLPVLYEFEHH-ARGIIVKPRTDGADHGDY 495
 DB 414 KDLFLDLADLLFGVPSVNVARHRDAGAPTYMYEYRYSFSSDMRPKTVIGHGDEIF 473
 QY 496 FLFGPPATGSLMSKEKALSLQMKYWANFARTGNPDGMLPCWPRYKDEKYLQDFTT 555
 DB 474 SVLGAPFLKEGATEETKLSQVWKYWANFARNPNNGEGLPQWPAYDYKEGYLQIGATT 533
 QY 556 RVGKMLKEKQAFWMSLY--QSORPEK 580
 DB 534 QAAQKLDKXEVAFWTELWAKEAPRE 560

RESULT 2
 US-08-845-295A-2
 ; Sequence 2, Application US/08845295A
 ; Patent No. 5817490
 ; GENERAL INFORMATION:
 ; APPLICANT: Hubbs, John C.
 ; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
 ; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
 ; TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eastman Chemical Company
 ; STREET: P.O. Box 511
 ; CITY: Kingsport
 ; STATE: Tennessee
 ; COUNTRY: USA
 ; ZIP: 37662-5075
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch disk
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/845,295A
 ; FILING DATE: 25-April-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/017,879
 ; FILING DATE: 17-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cheryl J. Tubach
 ; REGISTRATION NUMBER: 38,346
 ; REFERENCE/DOCKET NUMBER: 70432
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 423-229-6189
 ; TELEFAX: 423-229-1239
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 584 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; US-08-845-295A-2

Query Match 37.6%; Score 1169.5; DB 2; Length 584;
 Best Local Similarity 43.0%; Pred. No. 6.9e-111;
 Matches 249; Conservative 108; Mismatches 193; Indels 29; Gaps 13;
 QY 26 WILCWSLTLCLMAQALGALHTKRPQV-TKYGTLOGKQMHVG----KTPIQVFLGVPPS 80
 DB 2 WLL--PLVLTSLASSATWACQAPSPFVDTAQGRVLGKYVSLGLEAFTQPVAVFLGVPEA 59
 QY 81 RPPLGLIRFAPPPPPKGIKIRATTPPGCLQESWGQLASMYVST---RERYKWLRFPS 136
 DB 60 KPFLGSLRFAPPOPAEPWSEVKTYSYPPMCCDDPVVEQMTSDLFNFTGKELT-LRFS 118

QY 137 EDCLYLYNAYAPARPCDQPLPVMWFFPGAGIVGAASYESGSDLAAREK--VWLVFLQHR 194
 DB 119 EDCLYLYNTYTPADUTKGRFLFVMVWYHGGGLVLGGAPMYDGVVLAHAHENFTVVVVAQYR 178
 QY 195 LGIFLFLTDDSHARGNMGLLDQMAALRWQENIAAAGGDPGNVTLFGQS--AGAMSISG 252
 DB 179 LGIWGFFSTGDEHSGNMGHLDQVAALHWQENIANFGGDPGVTIFGESFTAGESVS 238
 QY 253 LMSPLASGLPHRAISQGTALFRLFITSNPLKVAKVAAHLAGNHNSTQI--LVNCLRA 310
 DB 239 LVLSPLAKNLPHRAISESGVALTVALKVKDKMAAKQIAVLGCKTITTSVAFTEFVHCLRQ 298
 QY 311 LSGTKVMRVSNKMRFLQNLNFORDEEIIWMSPPVVDGWIIPDDPLVLLTQ--KVSSVPY 368
 DB 299 KSEDELLDLTLMKFLTLDFHGDQRESHFPFLTVVDGVLVFKMPEEILAEKDFTFNTPY 358
 QY 369 LGVNNLEFNWLLPYIMKFPNLRQAMRKETITKMLNSTRLNLITKEQVPLV--VEEYLD 426
 DB 359 IVGINKQBFGLWLLPTMGFPLSEGLDKQATSLWKSYPITANIPPELTVPVATFTDKYL 418
 QY 427 NVNEHDKMLNRMMDIVQDATFVYATLQTAHYHRDAGLPVLYEFEHH--ARGIIVKP 483
 DB 419 GTDDPVKK--KDLFLDLMDGVVFGVPSVTVARQHRDAGAPTYMYEFOYRFSFSSDKETKP 476
 QY 484 RTDGADHGDYMYFLFGGPPATGLSMGKEKALSLQMKYWANFARTGNPDGMLPCWP--R 541
 DB 477 KTVIGDHGDEIFSVFGFPLKGDAPBEVSLSKTVMKFANFARSGNPNGEGLPHWPF 536
 QY 542 YNDEKYLQDFTTRVGMKLIKEXKQAFWMSLYQSORPEK 580
 DB 537 YDBEGYLQIGVNTQAAKRLKGEVAFWNDLLSKEAARK 575

RESULT 3
 US-09-140-933-2
 ; Sequence 2, Application US/09140933
 ; Patent No. 6022719
 ; GENERAL INFORMATION:
 ; APPLICANT: Hubbs, John C.
 ; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
 ; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
 ; TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eastman Chemical Company
 ; STREET: P.O. Box 511
 ; CITY: Kingsport
 ; STATE: Tennessee
 ; COUNTRY: USA
 ; ZIP: 37662-5075
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch disk
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/140,933
 ; FILING DATE: 27-August-98
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/017,879; 08/845,295
 ; FILING DATE: 17-May-96; 25-April-97
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cheryl J. Tubach
 ; REGISTRATION NUMBER: 38,346
 ; REFERENCE/DOCKET NUMBER: 70432
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 423-229-6189
 ; TELEFAX: 423-229-1239
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 584 amino acids
 ; TYPE: Amino Acid

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; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-09-140-933-2

Query Match          37.6%; Score 1169.5; DB 3; Length 584;
Best Local Similarity 43.0%; Pred. No. 6.9e-111;
Matches 249; Conservative 108; Mismatches 193; Indels 29; Gaps 13;

QY 26 WILCWSLTLCLMAQTALGALHTKRPQV-TKYGTLOGKQMHVG-----KTIQVFLGVDPFS 80
Db 2 WLL--PLVLTSLASSATWAGQSPVVDTAQGRVLGKYVSLGLELAFTQPVAVFLGVDPFA 59

QY 81 RPLGLILRFAPPPPEPWKIRDTATYPGCLQESWGQSLASMYST----KTIQVFLGVDPFS 136
Db 60 KPPLGSLURFAPPAEPWSFKVNTTSYPPMCCODPVVEQMTSLDFNFTGKERLT-LFES 118

QY 137 EDCLYLNVYAPARAPGDPQLPMVMFPGGAFIVGAASSYEGSDLAAREK--VVLVFLQHR 194
Db 119 EDCLYLNIYTPADLTRKGRLPVMMVHGGGLVGGAPMYDGVVLAHAHENFTVVVAIQYR 178

QY 195 LGIFGFLSTDSDSHARGNKGILLDQAAALRWQENIAAFGGDPGNVTLFGQS--AGAMSISG 252
Db 179 LGIWGFFSTGDEHSRGNWGHLDQAAALHWQENIANFNGDPSGVTIFGESFTAGGESVSV 238

QY 253 LKMSPLASGLFHRAISQSGTALFRLFTTSNPLKVAKKVAHLACGNHNSIQI--LVNCLRA 310
Db 239 LVLSPLAKNLFHRAISSEGVALTVALVRKDKMAAKQIAVLACGKTTTSVAVTFVHCLRQ 298

QY 311 LSGTKVMRVSNKRFLOINQFORDPEEIIWSMSPVVDGVVTPDDPLVLLTQG--KVSSVPY 368
Db 299 KSEDELLDLTLKKKFLTLDFHGDQRESHFPFLPTVVDGVLLPKMPEELAEKDFTFNTVPY 358

QY 369 LLGVNNELEFNWLLPYIMKFLNQRQAMRKETITKMLWSTRTLLNITKEQVPLV--VVEYLD 426
Db 359 IVGINKQEFGWLLPTMNGFPLSEGKLDOKTATSLWKSYPIANIPEELTPVATFTDKYLG 418

QY 427 NVNEHDKMLRNRMMDIVQDATFYATLQTAHYHRDAGLPVLYVEFEHH--ARGIIVKP 483
Db 419 GTDDPVKK--KDLFLDLMGDVVFGVPSVTVARQHRDAGAPTMYVEFYRPSFSSDKFTKP 476

QY 484 RTDGADHDGDEMFLFGGPFATGLSMGKEKALSLOMKYKWFANFARTGNPDGNLPCWP--R 541
Db 477 KTVIGDHGDEIFSVFGFPLKGDAPEEVLSKTVKFWANFARSGNPNGEGLPHPPTM 536

QY 542 YNKDEKYLQDLFTTRVGMKLEKKMAFWMSLYQSQRPEK 580
Db 537 YDQEGYLIQVNTQAARKLGEEVAFWNDDLKSEAAKK 575

RESULT 4
US-09-146-661-2
; Sequence 2, Application US/09146661
; Patent No. 6136575
; GENERAL INFORMATION:
; APPLICANT: Hubbs, John C.
; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Chemical Company
; STREET: P.O. Box 511
; CITY: Kingsport
; STATE: Tennessee
; COUNTRY: USA
; ZIP: 37662-5075
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146.661

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; FILING DATE: 03-September-98
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,879; 08/845,295
; FILING DATE: 17-May-96; 25-April-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Cheryl J. Tubach
; REGISTRATION NUMBER: 38,346
; REFERENCE/DOCKET NUMBER: 70432
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 423-229-6189
; TELEFAX: 423-229-1239
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-09-146-661-2

Query Match          37.6%; Score 1169.5; DB 3; Length 584;
Best Local Similarity 43.0%; Pred. No. 6.9e-111;
Matches 249; Conservative 108; Mismatches 193; Indels 29; Gaps 13;

QY 26 WILCWSLTLCLMAQTALGALHTKRPQV-TKYGTLOGKQMHVG-----KTIQVFLGVDPFS 80
Db 2 WLL--PLVLTSLASSATWAGQSPVVDTAQGRVLGKYVSLGLELAFTQPVAVFLGVDPFA 59

QY 81 RPLGLILRFAPPPPEPWKIRDTATYPGCLQESWGQSLASMYST----KTIQVFLGVDPFS 136
Db 60 KPPLGSLURFAPPAEPWSFKVNTTSYPPMCCODPVVEQMTSLDFNFTGKERLT-LFES 118

QY 137 EDCLYLNVYAPARAPGDPQLPMVMFPGGAFIVGAASSYEGSDLAAREK--VVLVFLQHR 194
Db 119 EDCLYLNIYTPADLTRKGRLPVMMVHGGGLVGGAPMYDGVVLAHAHENFTVVVAIQYR 178

QY 195 LGIFGFLSTDSDSHARGNKGILLDQAAALRWQENIAAFGGDPGNVTLFGQS--AGAMSISG 252
Db 179 LGIWGFFSTGDEHSRGNWGHLDQAAALHWQENIANFNGDPSGVTIFGESFTAGGESVSV 238

QY 253 LKMSPLASGLFHRAISQSGTALFRLFTTSNPLKVAKKVAHLACGNHNSIQI--LVNCLRA 310
Db 239 LVLSPLAKNLFHRAISSEGVALTVALVRKDKMAAKQIAVLACGKTTTSVAVTFVHCLRQ 298

QY 311 LSGTKVMRVSNKRFLOINQFORDPEEIIWSMSPVVDGVVTPDDPLVLLTQG--KVSSVPY 368
Db 299 KSEDELLDLTLKKKFLTLDFHGDQRESHFPFLPTVVDGVLLPKMPEELAEKDFTFNTVPY 358

QY 369 LLGVNNELEFNWLLPYIMKFLNQRQAMRKETITKMLWSTRTLLNITKEQVPLV--VVEYLD 426
Db 359 IVGINKQEFGWLLPTMNGFPLSEGKLDOKTATSLWKSYPIANIPEELTPVATFTDKYLG 418

QY 427 NVNEHDKMLRNRMMDIVQDATFYATLQTAHYHRDAGLPVLYVEFEHH--ARGIIVKP 483
Db 419 GTDDPVKK--KDLFLDLMGDVVFGVPSVTVARQHRDAGAPTMYVEFYRPSFSSDKFTKP 476

QY 484 RTDGADHDGDEMFLFGGPFATGLSMGKEKALSLOMKYKWFANFARTGNPDGNLPCWP--R 541
Db 477 KTVIGDHGDEIFSVFGFPLKGDAPEEVLSKTVKFWANFARSGNPNGEGLPHPPTM 536

QY 542 YNKDEKYLQDLFTTRVGMKLEKKMAFWMSLYQSQRPEK 580
Db 537 YDQEGYLIQVNTQAARKLGEEVAFWNDDLKSEAAKK 575

RESULT 5
US-09-150-515-2
; Sequence 2, Application US/09150515
; Patent No. 6271006
; GENERAL INFORMATION:
; APPLICANT: Hubbs, John C.
; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of

```

```

; TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Chemical Company
; STREET: P.O. Box 511
; CITY: Kingsport
; STATE: Tennessee
; COUNTRY: USA
; ZIP: 37662-5075
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/150,515
; FILING DATE: 09-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,879; 08/845,295
; FILING DATE: 17-May-96; 25-April-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Cheryl J. Tubach
; REGISTRATION NUMBER: 38,346
; REFERENCE/DOCKET NUMBER: 70432
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 423-229-6189
; TELEFAX: 423-229-1239
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; US-09-150-515-2

Query Match 37.6%; Score 1169.5; DB 3; Length 584;
Best Local Similarity 43.0%; Pred. No. 6.9e-111;
Matches 249; Conservative 108; Mismatches 193; Indels 29; Gaps 13;

QY 26 WILCWSITLCMAOTALGALHTRKQV - KYGTLOGKQMHVG - KTPIQVFLGVPS 80
DB 2 WLL--PLVATSLASSATWAGPASPVPVDTAQRVLGKYVSLGLAFTQPAVFLGVPTA 59

QY 81 RPPGLILREAPPEPEPEKGIARDATTYPGCLQESGQLASMYST - RERYKWLRS 136
DB 60 KPPLGLSRFPAPQAEPSFVKNTISYPNCCQDPVVEQMTSDLTFTNFGKERLT - LEFS 118

QY 137 EDCILYLVNYPAPAPGDPOLPVMVWPFPGAFIVGAASSYEGSDLAAREK - VVLVFLQHR 194
DB 119 EDCILYLVNYPADLTKEGRPLPVMVWIHGGGLVGGAPMTDGVVLAHAENFTVVAIQYR 178

QY 195 LGIFGLPLSTDDSHARGNWGLDQMAALRWQENIAAFGGDPGVNTLFGQS - AGAMSISG 252
DB 179 LGIWFSTGDSHRGNWGLDQVAALHWQENIANFGDPGVNTLFGSFTAGSESIV 238

QY 253 LMSPLASGLFHRAISQSGTALFRFLTITSNPLKVAHVLAAGCNHNSQI - LVNCLRA 310
DB 239 LVLSPLAKNLFHRAISEGVALTVALVRKMDKAAQIAVLACGKTTTSVATFVHCLRQ 298

QY 311 LSGTKMVRNKNRFLQNLNFORPELIIWSMSPVVDGVIPDDPLVLLTQ - KVSVPY 368
DB 299 KSEDELLDLTKMKFLTLDFHGDQRESHPLFTVWDGVLLPKMPEBILAEKDTFTNTPY 358

QY 369 LLGVNNLEFNNLLPYIMKFFLNQARKKETITKMLSTRLLNITKEQVPLV - VEEYLD 426
DB 359 IVGINKQEFGLLPTWMPFLSGKLDQKTAISLLAKSPIANIPELTPVATFDTKYL 418

QY 427 NVNEHWKMLNRNMDIVQDATFVYATLQTAHVHRDAGLPVLYEPEHH - ARGIIVK 483
DB 419 GTDDPVKK - KDLFLDLMGVWFVGPVSVTARQHRDAGAPTYMYEQYRFSFSDKFTK 476

QY 484 RTDGADHGDMEYFLFGPPATGLSMGKEKALSLOMKYKWNFARTGNPNNDGNLPCWP - R 541

; TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Chemical Company
; STREET: P.O. Box 511
; CITY: Kingsport
; STATE: Tennessee
; COUNTRY: USA
; ZIP: 37662-5075
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/150,515
; FILING DATE: 09-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,879; 08/845,295
; FILING DATE: 17-May-96; 25-April-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Cheryl J. Tubach
; REGISTRATION NUMBER: 38,346
; REFERENCE/DOCKET NUMBER: 70432
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 423-229-6189
; TELEFAX: 423-229-1239
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; US-09-150-515-2

Query Match 36.8%; Score 1145; DB 4; Length 581;
Best Local Similarity 42.8%; Pred. No. 2.2e-108;
Matches 249; Conservative 91; Mismatches 186; Indels 56; Gaps 13;

QY 11 LPSLLPTAGAGSMRWILCWSITLCMAOTALG - ALHTRKQVTVKGTLOGKQ 63
DB 1 MPQGTSSASQW - CFFLIL - QPLHGRQMGKTGPSAEGPQRTNLRLGWIQKQ 50

QY 64 MHV - GKTPIQVFLGVPSRPPGLILRFAPPEPEPEKGIARDATTYPGCLQESWGLAS 121
DB 51 VTVLGSPVPVNVFLGVFPFAAPPLGSLAFTNPQPPASPDNLREATSYENLCLQSEWLLD 110

QY 122 MYSTRERYKWLRSSECLYLVNYPAPAPGDPOLPVMVWPFPGAFIVGAASSYEGSDLA 181
DB 111 QHM - LKVHPKFGVSECLYLVNYPAPADTGSKLPLVWVFPFGAFITGSASIFDGSALA 169

QY 182 AREKVLVFLQHRIGIFGFTSTDDSHARGNWGLDQMAALRWQENIAAFGGDPGVNTLF 241
DB 170 AYEDVLVVVQYRIGIFGFTTWDQHPAGNAPKQVQVLAALSWQKNEFFGGDPSSVTIP 229

QY 242 GQSGAGMSISGLMSPASGLFHRAISQSGTALFR - FITSNPLKVAHVLAAGC 296
DB 230 GESAGATSVSLLSPMAKGLFHRAIMESGVAIIPYLEAHDEYKSEDLQV - VAHPCGN 286

QY 297 NHNSTQILNCLRALSGTKMVRNKNRFLQNLNFORPELIIWSMSPVVDGVIPDDPLV 356
DB 287 NASSEALLCLRTKPSKELLTISQTK - SFTRVUDGAFPPNEPLD 331

QY 357 LLTGKVSVPVLLGVNNLEFNNLLPYIMKFFLNQARKKETITKMLSTRLLNITKEQ 416
DB 332 LLSQKAFKAIPSIIGVNNHECGFLLP - MKEAPEILSGSNKSLALHLI - QNTLHIPPOY 387

QY 417 VPLVVEYLVNVEHDKMLNRNMDIVQDATFVYATLQTAHVHRDAGLPVLYEPEHH 476
DB 388 LHLVANFYFH - DKHSUTEIRDSLLDGLGVFFVPALITARVHRDAGAPVYEFHRP 445

QY 477 RGI - IVKPRTDGADHGDMEYFLFGPPATG - LSMGKEKALSLOMKYKWNFARTG 529
DB 446 QCFEDTKPAFVKADHADNVRVFGGAFKGDIVNFEGETEEKLLSRKMKYKWNFARTG 505

QY 530 NPNDGNLPCWPYRKNKDEKYLQLOFTTRVGMKLEKQKAFWMS 571

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; Sequence 26, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-26

Query Match 31.6%; Score 983.5; DB 3; Length 454;
Best Local Similarity 43.6%; Pred. No. 5.6e-92;
Matches 196; Conservative 91; Mismatches 158; Indels 5; Gaps 4;

QY 137 EDCLYNYVAPARAPDQPLPVMVFPFGAFIVGAASYESGDLAAREKVVLFQHLRLG 196
DB 1 EHCLYLYNITPADLTKNRLPVMVHGGGLMVGAASYDGLAALAHENVVVVTIYRLG 60

QY 197 IPGFILSTDSDSHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMS 256
DB 61 IWGFSTGDEHSRGNWGHLDQVAALRWQDNIAISFGGNPGSVTIFGESAGGESVSVLVS 120

QY 257 PLASGLFRAISQSQTALFRLFITSNPLK-VAKKVAHLAGCNHNSTQILVNCRLALSQTK 315
DB 121 PLAKNLFRAISESGVALTSVLVKGVKPLABQIAITAGCKTTTSAAMVHCLRQKTBEE 180

QY 316 VMRSVKNRFLQNFORDPPEELIWSMSPVGVGVITPDDPLVLLTQCKVSSVPYLLGVNVL 375
DB 181 LLETTLKIGNSYLWYRETQREESTLLGTVIDGMLLKTPEELQERNFHTVPYMGVGNKQ 240

QY 376 EFNWLLP-YIMKFLPNRQAMRKETITKMLWSTRTLNITKEQVPLVVEYLDNVNNEHDWK 434
DB 241 EFGWLPIMOLMSYPLSEGLDQKXTAMSLGSPILFAIAKELIPEATEKYLGGTD-DTV 298

QY 435 MLNRMMMDIVQDATFYATLQTAHYHRDAGLPVLYEPEHH-ARGIIVKPRTDGADHGDE 493
DB 299 KKKDLILDLIADVMFGVPSVIVARNHRDAGATYMYEFQYRPSFSSDMKPKTVIGDHGDE 358

; Sequence 26, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-26

Query Match 36.4%; Score 1133; DB 3; Length 539;
Best Local Similarity 41.3%; Pred. No. 3.3e-107;
Matches 227; Conservative 115; Mismatches 177; Indels 30; Gaps 10;

QY 46 HTKEPVVTKYKGLQKQHVKG-----TPIQVFLGVPSRSEPLGILLRAPPPEPP 97
DB 1 HPSAPPVV--DITVKGVL--GKFSLEGFAQVAVFLGVFFAKPLGSLRFPAPPAS 55

QY 98 WKGIRDATTYPGCLQ--SWGOLASMYVSTRERYKWLRFSEDCLYNIVYAPARAPDQ 155
DB 56 WSHVKNITTSYPPMCSSDAVSGHMLSELFTRNKENIP-LKPESEDCLYNIVTPADLTGR 114

QY 156 LPVMVFPFGAFIVGAASYESGDLAAREKVVLFQHLRIGIFGLSTDSDSHARGNWGL 215
DB 115 LPVMVHGGGLMVGGASTYDGLSAHENVVVVTIYRLGIGGPGFNIDE-----L 166

QY 216 DQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFRAISQSQTALF 275
DB 167 FLAVNRWQDNIAFNGDGGSVTIFGESAGGQSVLILSLPTKMLFRAISESGVALL 226

QY 276 RLFTTSNPLKVAKVAHLAGCNHNSTQILVNCRLALSQTKVMRSVKNRFLQNFORDPE 335
DB 227 SSLFRKNTKSLAEKIAIEAGCKTTTSAVMVHCLRQKTEEBELMEVTLKMKFVALDLVGD 286

QY 336 ELIWSMSPVGVGVITPDDPLVLLTQCKVSSVPYLLGVNNEFNWLLP-YIMKFLPNRQAM 394
DB 287 ENTAFLLTVIDGVLLPKAPAEIYEKKYNMLPYVGINQOEFGWILPMQMLGFLSEGLK 346

QY 395 RKETITKMLWSTRTLNITKEQVPLVVEYLDNVNNEHDWKVLRNRMMDIVQDATFYATL 454
DB 347 DQKATTELLMKSYPVNVSKELTPVATEKYLGGTDDPVKK-KDLFLDLMLADLLFGVPSV 404

QY 455 QTAHYHRDAGLPVLYEPEHH-ARGIIVKPRTDGADHGDEMYFLFGPPFATGLSMGKEKA 513
DB 405 NVARHHRDAGAPTMYRYRPSFSSDMRPKTVIGDHDGEIFSVLGAFFLKEGATEEIK 464

QY 514 LSLQMKYKWFANFARTGNPDNGLPCWPRYNKDEKYLQLDFTTRVGMKLEKQKQAFWMSLY 573
DB 465 LSKVMYKWFANFANGPNSEGLPQWPAIDYKEGYLQIGATTQAAQKLKQKEVAFWTELW 524

QY 574 --QSORPEK 580
DB 525 AKEAAPRE 533

RESULT 8
US-08-446-100-26
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Db 1 EHCLYLNIVTPADLTCKNRLPVMMVTHGGGLVMVGAASYDGLAALAHENVVVVTIQYRLG 60
QY 197 IFGFLSTDDSHARGNGLDQVAALRWQENIAAFGGDPGNVTLFGOSAGASISGLMMS 256
Db 61 IWGFSTGDEHSRGNWGHLDQVAALRWVQDNIAFSGNPGSVTIIFGSAAGSVSVLVLS 120
QY 257 PLASGLFHRAISOGTALFRLFTITSNPLK-VAKKVAHLAGCNHNSTQILVNCRLALSGTK 315
Db 121 PLAKNLFHRAISGVALTSVLVKGDVKPLAEQIAITAGCKTTTSAAMVHCLRQKTEEE 180
QY 316 VMRYSNKMFRLQNFORDPEEIIWMSFVVDGVVVDVLLVLTQGVSSVYLLGVNVL 375
Db 181 LLETTLKIGNSYLWYRETQRESHLLGTVIDGMLLKTPEELQRENFHTVPMVGINKQ 240
QY 376 EFNWLLP-YIMKFLPNRQAMEKETTITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWK 434
Db 241 EFGWLPFMQLMSYPLSEGQDQKTAMSLGSPFLFAIAKELIPEATEKYLGGTD--DTV 298
QY 435 MLNRNMDIVODATFVYATLQTAHYHRDAGLPVLYIEFEHH-ARGIIVKPRTDGADHGDE 493
Db 299 KKKDLILDIAVDMFVPSVIVARNHRDAGAPTYMYEFQYRFSFSDMKPKTVIGDHGDE 358
QY 494 MYFLFGGPFATGLSMGKEKALSQMKMYANFARTGNPDGNLPCWPRYNKDEKYLQDLF 553
Db 359 LFSVFGAPFLKEGASEEIEIRLSKVMKFWANFARNPNKGLPHWPEYNQKEGYLQIGA 418
QY 554 TTRVGMKLKKEKMAFWMSLYQSQRPEKQ 583
Db 419 NTQAAQKLKDEKVAFTNLFKAKKAVEKPPQ 448

RESULT 11
US-08-446-100-27
; Sequence 27, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
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; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-27

Query Match 31.5%; Score 981.5; DB 3; Length 454;
Best Local Similarity 43.6%; Pred. No. 8.9e-92;
Matches 196; Conservative 91; Mismatches 158; Indels 5; Gaps 4;

QY 137 EDCLYLNIVYAPAPGDPQLPVPVMMVTHGGGLVMVGAASYDGLAALAHENVVVVTIQYRLG 196
Db 1 EHCLYLNIVYAPADLTCKNRLPVMMVTHGGGLVMVGAASYDGLAALAHENVVVVTIQYRLG 60
QY 197 IFGFLSTDDSHARGNGLDQVAALRWQENIAAFGGDPGNVTLFGOSAGASISGLMMS 256
Db 61 IWGFSTGDEHSRGNWGHLDQVAALRWVQDNIAFSGNPGSVTIIFGSAAGSVSVLVLS 120
QY 257 PLASGLFHRAISOGTALFRLFTITSNPLK-VAKKVAHLAGCNHNSTQILVNCRLALSGTK 315
Db 121 PLAKNLFHRAISGVALTSVLVKGDVKPLAEQIAITAGCKTTTSAAMVHCLRQKTEEE 180
QY 316 VMRYSNKMFRLQNFORDPEEIIWMSFVVDGVVVDVLLVLTQGVSSVYLLGVNVL 375
Db 181 LLETTLKIGNSYLWYRETQRESHLLGTVIDGMLLKTPEELQRENFHTVPMVGINKQ 240
QY 376 EFNWLLP-YIMKFLPNRQAMEKETTITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWK 434
Db 241 EFGWLPFMQLMSYPLSEGQDQKTAMSLGSPFLFAIAKELIPEATEKYLGGTD--DTV 298
QY 435 MLNRNMDIVODATFVYATLQTAHYHRDAGLPVLYIEFEHH-ARGIIVKPRTDGADHGDE 493
Db 299 KKKDLILDIAVDMFVPSVIVARNHRDAGAPTYMYEFQYRFSFSDMKPKTVIGDHGDE 358
QY 494 MYFLFGGPFATGLSMGKEKALSQMKMYANFARTGNPDGNLPCWPRYNKDEKYLQDLF 553
Db 359 LFSVFGAPFLKEGASEEIEIRLSKVMKFWANFARNPNKGLPHWPEYNQKEGYLQIGA 418
QY 554 TTRVGMKLKKEKMAFWMSLYQSQRPEKQ 583
Db 419 NTQAAQKLKDEKVAFTNLFKAKKAVEKPPQ 448

RESULT 12
US-08-446-100-28
; Sequence 28, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
```

```

; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-28

Query Match 31.4%; Score 977.5; DB 3; Length 454;
Best Local Similarity 43.6%; Pred. No. 2.3e-91;
Matches 196; Conservative 90; Mismatches 159; Indels 5; Gaps 4;

QY 137 EDCLYLVYAPARAPGDPQLPVWVFFGAFIVGAASSYEGSDLAAREKVLVFLQRLG 196
DB 1 EHCYLVNIYTPADLTCKNRLPVWVWIGHGHLVDGAASYDGLAAHENVVVTIQLRG 60

QY 197 IFGLSTDDSHARGNWGLDQMAALRWQENIAAFGGDPGNVTLFGOSAGAMSISGLMMS 256
DB 61 IWGFSTGDEHSRGNWGLDQVAALRWQDNIAAFGGNPGSVTFGESAGGESVSVLVLS 120

QY 257 PLASGLFHRAISQSGTALFRFLTSPNLK-VAKKVAHLACGNHNSCTILVNCRLALSGTK 315
DB 121 PLAKNLFHRAISESGVALTSVLVKGDVPLAQIAITAGCKTTTSAAMVHCLRQKTEE 180

QY 316 VMRVSNKMRFLQNFQDPDEEIIWMSPPVVDGVVIPPDDPLVLLTQGVKSSVPYLLGVNLL 375
DB 181 LLETTLKIGNSYLTWYRETQRESTLLGTVDGMLLKTPEELQRENFHFTVPYVGVINKQ 240

QY 376 EFNWLLP-YIMKPLNQAQMKETITKMLWSTRTLLNITKEQVPLVVEEYLDVNVNHDWK 434
DB 241 EFGWLIQWQLMSYPLSEGQDDQKATMSLLGSPILFAIAKELIPEATEKYLGGTD--DTV 298

QY 435 MLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYVEFEHH-ARGIIVKPRDTGDAGHDE 493
DB 299 KKXDLILDLIADVMFGVPSVIVARNHRDAGAPTYMVEFYQYRPSFSSDMKPKTVIGDHGE 358

QY 494 MYFLFGGPPATGLSMGKEKALSQMKYANFARTGNPDGNLPCWPRYNKDEKYLQDF 553
DB 359 LFSVFGAPFLKEGASEEIRLSXVWKFANFARNPNNGKGLPHWPEYNQKEGYLQIGA 418

QY 554 TTRVGMKLEKKKXAFWMSLYQSQRPEKQRQ 583
DB 419 NTQAAQKLKDKKEVAFWNLFAKXAVEKPPQ 448

```

RESULT 13

```

US-08-446-100-29
Sequence 29, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-May-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenn
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-29

```

```

Query Match 31.4%; Score 977.5; DB 3; Length 454;
Best Local Similarity 43.6%; Pred. No. 2.3e-91;
Matches 196; Conservative 90; Mismatches 159; Indels 5; Gaps 4;

QY 137 EDCLYLVYAPARAPGDPQLPVWVFFGAFIVGAASSYEGSDLAAREKVLVFLQRLG 196
DB 1 EHCYLVNIYTPADLTCKNRLPVWVWIGHGHLVDGAASYDGLAAHENVVVTIQLRG 60

QY 197 IFGLSTDDSHARGNWGLDQMAALRWQENIAAFGGDPGNVTLFGOSAGAMSISGLMMS 256
DB 61 IWGFSTGDEHSRGNWGLDQVAALRWQDNIAAFGGNPGSVTFGESAGGESVSVLVLS 120

QY 257 PLASGLFHRAISQSGTALFRFLTSPNLK-VAKKVAHLACGNHNSCTILVNCRLALSGTK 315
DB 121 PLAKNLFHRAISESGVALTSVLVKGDVPLAQIAITAGCKTTTSAAMVHCLRQKTEE 180

QY 316 VMRVSNKMRFLQNFQDPDEEIIWMSPPVVDGVVIPPDDPLVLLTQGVKSSVPYLLGVNLL 375
DB 181 LLETTLKIGNSYLTWYRETQRESTLLGTVDGMLLKTPEELQRENFHFTVPYVGVINKQ 240

QY 376 EFNWLLP-YIMKPLNQAQMKETITKMLWSTRTLLNITKEQVPLVVEEYLDVNVNHDWK 434
DB 241 EFGWLIQWQLMSYPLSEGQDDQKATMSLLGSPILFAIAKELIPEATEKYLGGTD--DTV 298

QY 435 MLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYVEFEHH-ARGIIVKPRDTGDAGHDE 493
DB 299 KKXDLILDLIADVMFGVPSVIVARNHRDAGAPTYMVEFYQYRPSFSSDMKPKTVIGDHGE 358

QY 494 MYFLFGGPPATGLSMGKEKALSQMKYANFARTGNPDGNLPCWPRYNKDEKYLQDF 553
DB 359 LFSVFGAPFLKEGASEEIRLSXVWKFANFARNPNNGKGLPHWPEYNQKEGYLQIGA 418

QY 554 TTRVGMKLEKKKXAFWMSLYQSQRPEKQRQ 583
DB 419 NTQAAQKLKDKKEVAFWNLFAKXAVEKPPQ 448

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RESULT 14

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US-10-023-515-4
Sequence 4, Application US/10023515
Patent No. 6664091
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Imaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

```

```
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 574
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-10-023-515-4

Query Match      29.2%; Score 908.5; DB 4; Length 574;
Best Local Similarity 39.6%; Pred. No. 4.1e-84;
Matches 226; Conservative 87; Mismatches 181; Indels 77; Gaps 24;

QY 67 GKTPIQVFLGVPSPRDLGLIRAPPPEPPEPKGIRDAITPPGCLQ-ESWG-QLASMY 123
Db 13 GEOSVSYFLGIPAEPPVGNLRKAPQYKEPNSDVLDAIKYPPSCLODDDFGFSLSDLK 72

QY 124 VSTR-----ERYKWLRFSEDCLYLVNYPAPAPGDPQLPVMWFFGGAPIVGAAS--- 174
Db 73 VALKMLSLGNKLVGLKLSDCLYLVNYPKNTKPNKLPFWVMYIRGGGFMFGSGHSLPL 132

QY 175 --YEGSLAAREKVLVFLQHRIGIFGLSTDDSH--ARGNWGLLDQMAALRWVQENIAA 230
Db 133 SLVDGESLAREGNVIVVINSIRLPGIFLSTGDKLPFGSGNYGLLQRLALKVQDNIAA 192

QY 231 FGDGPGNVTLFGSAGAMSISGLMMS-----PLASGLPHRAISQSGTAL--PRLFITSN 282
Db 193 FGDGPNVITFGESAGAASVSLLLSNGGDNPPSSKGLPHRAISQSGSALLSPWAIQSEN 252

QY 283 PLKVAKVLAHLAGNHNSTQILNCLRALSGTKVMRVSNKMRFLQNLNFORDP--EELIWSM 341
Db 253 ARGAKELARLLGNETSSSELDDCLRSKSAEELLEATRSF----LFEYVPPFLPLFLAP 308

QY 342 SPVVDG----VTPDDPLVLLTGKVSVPYLLGVNNLEFNMLLPYIMKFFPLNRQA--- 393
Db 309 GPVVDGDDAEAFPEDEPEELIKEGFADVPYLLIGVTKDEGG---YFAAMLLNASSKGE 364

QY 394 --MKET-----ITKMLNSTRLTNITKEQVPL---VVEYLDNVDNHDWMLNRM 440
Db 365 DELKKTNPDPVWLELLLYLLFYASEALNI-KDMDDLADKVLKYPGSDVDDFSVESRKNL 423

QY 441 MDIVQDATFVYATLQTAHYH-RDAGLPVLYVEFEHAR-GI-----IVKPRTDGADHGD 492
Db 424 QDMLTDLFLKCPTRVAADLHAKHGSPVYAVVFDHPASFGLGQFLAKRVDPFEGGAVHGD 483

QY 493 EMYFLFGGPFAT---GLSMGKEKALSQMMKYWANFARTGNPNNDG---NLPQWPRYNKD 545
Db 484 BIFFVFGNPLLEQLYKATEBEESKSSKTMNYWANFAKTGNPNNGTSNGLVVMKPYTSE 543

QY 546 E-KY-LQLDFTTRVMKLEKKK-----MAFW 569
Db 544 BQVSLLLLTITTAQKLKARDPRKVLGNFW 574
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RESULT 15
US-09-491-356C-21
Sequence 21, Application US/09491356C
Patent No. 6566061
GENERAL INFORMATION:
APPLICANT: Philibert, Robert A.
APPLICANT: Gibbs, Edward I.
APPLICANT: Delisi, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REFERENCE: 9465.6US11
CURRENT APPLICATION NUMBER: US/09/491,356C

Query Match      27.3%; Score 849; DB 4; Length 836;
Best Local Similarity 33.2%; Pred. No. 1e-77;
Matches 215; Conservative 92; Mismatches 191; Indels 150; Gaps 21;

QY 30 WSLTLCILM---AO-----TALGALHTKR-POVVTYKVTGLGQKQMHVGT 69
Db 2 WLLALCLVLAGARGGGGPGGPGGLGSLGSEERFPVNTAYGRVGRVERELNNE 61

QY 70 ---PIQVFLGVFPPRPLGILRPAPPPEPPPEPKGIRDAITPPGCLQESWQCL----- 119
Db 62 ILGPVVQFLGVYATPPLGARRFQPPAPASWPGVRNATTLPPACPNLHGALPALMLPV 121

QY 120 -----ASMVSTREYKWLRFSEDCLYLVNYPAPAR-----APGDPQL-- 156
Db 122 WFTDNLEAAATVQNQ-----SEDCLYLVNLYPTEDGPLTKRDBATLNPPTDIRD 173

QY 157 ---PVMWFFGGAPIVGAASYESGSLAAREKVLVFLQHRIGIFGLSTDDSHARGNW 212
Db 174 SGKXPMVFLFHGGSNMEGTGNMFDGSLAAYGNVIVATLNYRLGVGLSTGDOAAKGY 233

QY 213 GLDDQMAALRWVQENIAAFGGDPGNVTLFGSAGAMSISGLMMSPLASGLPHRAISQSGT 272
Db 234 GLDDQIQLRMLSENIAHFGGDPERITIFGSGAGASCNVLLLSHSHSGLFQKALAQSGT 293

QY 273 ALFRLFITSNPLKVAKVLAHLAGNHNSTQILNCLRALSGTKVMRVSNKMRFLQNLNFOR 332
Db 294 AISSNSVNYQPLKYTRLLAAKVGCDREDSTEAVECLRRKKSREL-----VDQDV 342

QY 333 DPEEIIWSMSPVVDGVVIPPDDPLVLLTGKVSVPYLLGVNNLE----- 376
Db 343 QPARYHIAFGPVVDGVVDVDDPEILMQQGEFLNYDMLIGVNAQGEGLKVEDESSEDGVS 402

QY 377 ---FNW---LLPYIMKFPNLRQAMRKETITKMLWSTRLTNITKEQVPLVVEEYLDNVN 429
Db 403 ASAFDFTVSNFVDNLYGYPEGKDVLR-ETIKFM-----YTDWAD 440

QY 430 EHDWMLNRNMDIVQDATFVYATLQTAHYHHDAGLPVLYFEFEH--ARGLIIVKPRTDG 487
Db 441 RONGEMRRKTLLALFTDQWVAPAVATAKLHADYQSPVYFYTFYHHCQAE--RPEWAD 497

QY 488 ADHGDEMYFLFGGPF--ATGL---SMGK-EKALSQMMKYWANFARTGNPDGNLP---- 537
Db 498 AAAGDELPYVFGVPMVVGATDLPFCNFSKNDVMSLAVMTYTNFTAKTGDPNQ-PVPQDTK 556

QY 538 -----CWPRYN-KDEKYLQLDFTTRVGMKLEKKQMAFWMSL 572
Db 557 FIHTKENRFEVWVSKFNSKEQYLHGLKPRVRDNYRANKVAFWLEL 604
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Search completed: August 3, 2004, 22:29:22
Job time : 20 secs

QY 181 AAREKVLVFLQHRLLGIFGLSTDDSHARGNWGLDDMAALRWVOENIAAFGGDPGNVTL 240
DB 181 AAREKVLVFLQHRLLGIFGLSTDDSHARGNWGLDDQVAALRWVOENIAAFGGDPGNVTL 240
QY 241 FQSAGAMISISGLMSPPLASGLFHRAISQSCTALPRLBITSNPLKVAKKVAHLACGNHNS 300
DB 241 FQSAGAMISISGLMSPPLASGLFHRAISQSCTALPRLBITSNPLKVAKKVAHLACGNHNS 300
QY 301 TQILVNCRLALSGTKVMRSNKMRFQNLNFORDEEIIWSMSPVVDGWIIPDDPLVLLTQ 360
DB 301 TQILVNCRLALSGTKVMRSNKMRFQNLNFORDEEIIWSMSPVVDGWIIPDDPLVLLTQ 360
QY 361 GKVSVPYLLGVNLLFNWLLPYIMKFPNQAQMKETITKMLWSTRTLLNITKEQVPLV 420
DB 361 GKVSVPYLLGVNLLFNWLLPYIMKFPNQAQMKETITKMLWSTRTLLNITKEQVPLV 420
QY 421 VEEYLDNVNHDWKMLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHHARGII 480
DB 421 VEEYLDNVNHDWKMLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHHARGII 480
QY 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540
DB 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540
QY 541 RYNKDEKYLQDFTTRVGMKLEKEMAFWMSLYQSQRPEKORQF 584
DB 541 RYNKDEKYLQDFTTRVGMKLEKEMAFWMSLYQSQRPEKORQF 584

RESULT 2

US-10-343-593-10
; Sequence 10, Application US/10343593
; Publication No. US20040110259A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;
; APPLICANT: BRUNS, Christopher M.; DAS, Debopriya;
; APPLICANT: DELEGANE, Angelo M.; DING, Li;
; APPLICANT: ELLIOT, Vicki S.; GANDHI, Ameena R.;
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.;
; APPLICANT: KAN, Farrah A.; LAL, Preeti G.;
; APPLICANT: LEE, Sally; LU, Dyung Alina M.;
; APPLICANT: LU, Yan; ARVIZU, Chandra S.;
; APPLICANT: RAMKOMAR, Jayalaxmi; RING, Huijun Z.;
; APPLICANT: SANJANWALA, Madhusudan M.; TANG, Y. Tom;
; APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael;
; APPLICANT: TRIBOULEY, Catherine M.; CHAWLA, Narinder K.;
; APPLICANT: WARREN, Bridget A.; YANG, Junming;
; APPLICANT: YAO, Monique G.; YUE, Henry
; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
; FILE REFERENCE: PI-0185 USN
; CURRENT APPLICATION NUMBER: US/10/343,593
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US 60/223,055
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,728
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/226,440
; 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/228,067
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,063
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/232,244
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/234,269
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 584
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7478588CD1
US-10-343-593-10

Query Match 100.0%; Score 3112; DB 16; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.5e-289;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESTVLPSTVLSLLPTAGAGSMRWILCWSLTLCLMAQTALGALHTRPQVVTKYGTQ 60
DB 1 MESTVLPSTVLSLLPTAGAGSMRWILCWSLTLCLMAQTALGALHTRPQVVTKYGTQ 60
QY 61 GKQMHVGKTIQOVFLGVFPSPPLGILRFAPPEPEPKGIRDATTYPGCLQESWGOLA 120
DB 61 GKQMHVGKTIQOVFLGVFPSPPLGILRFAPPEPEPKGIRDATTYPGCLQESWGOLA 120
QY 121 SMYVSTRERYKWLRFSEDCLYLNVYAPARPGDPQLPVMWFFPGGAFIVGAASVEGSDL 180
DB 121 SMYVSTRERYKWLRFSEDCLYLNVYAPARPGDPQLPVMWFFPGGAFIVGAASVEGSDL 180
QY 181 AAREKVLVFLQHRLLGIFGLSTDDSHARGNWGLDDMAALRWVOENIAAFGGDPGNVTL 240
DB 181 AAREKVLVFLQHRLLGIFGLSTDDSHARGNWGLDDQVAALRWVOENIAAFGGDPGNVTL 240
QY 241 FQSAGAMISISGLMSPPLASGLFHRAISQSCTALPRLBITSNPLKVAKKVAHLACGNHNS 300
DB 241 FQSAGAMISISGLMSPPLASGLFHRAISQSCTALPRLBITSNPLKVAKKVAHLACGNHNS 300
QY 301 TQILVNCRLALSGTKVMRSNKMRFQNLNFORDEEIIWSMSPVVDGWIIPDDPLVLLTQ 360
DB 301 TQILVNCRLALSGTKVMRSNKMRFQNLNFORDEEIIWSMSPVVDGWIIPDDPLVLLTQ 360
QY 361 GKVSVPYLLGVNLLFNWLLPYIMKFPNQAQMKETITKMLWSTRTLLNITKEQVPLV 420
DB 361 GKVSVPYLLGVNLLFNWLLPYIMKFPNQAQMKETITKMLWSTRTLLNITKEQVPLV 420
QY 421 VEEYLDNVNHDWKMLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHHARGII 480
DB 421 VEEYLDNVNHDWKMLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHHARGII 480
QY 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540
DB 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540
QY 541 RYNKDEKYLQDFTTRVGMKLEKEMAFWMSLYQSQRPEKORQF 584
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RESULT 3

US-09-978-295A-254
; Sequence 254, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/065364
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PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-13
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-05-06
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/ PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084640
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084598
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084600
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084627
 / PRIOR FILING DATE: 1998-05-07
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 / PRIOR APPLICATION NUMBER: 60/085582
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085700
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085689
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085579
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085580
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 9; Length 545;
 Best Local Similarity 80.3%; Pred. No. 3.6e-185;
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY	6	LPSTVLPBLLPTAGAGNMRILCWSLTLCLMAOTALGALHTRPQVVTYKYLQKQKH	55
DB	47	LGSTTPATTAPSSGFGTGLFGSKPATGFTLGTGNTGALHTRPQVVTYKYLQKQKH	106
QY	66	VGKTIQVFLGVFSPRPPLGILRFAPPEPPKPGKIRDATYPPG	110
DB	107	VGKTIQVFLGVFSPRPPLGILRFAPPEPPKPGKIRDATYPPGKSLALSPGMSAVAS	166
QY	111	-----CLOESWGQLASMYVSTRERYKWLRFSEDCLYLNY	145
DB	167	RLTATSASRVQASLLPQLPLSVMGYRC:QESWGQLASMYVSTRERYKWLRFSEDCLYLNY	226
QY	146	APARAPGDPQLPVMVFPFGGAFIVGAASSYEGSDLAAREKVLVFLQHLRIGIFGLSTDD	205
DB	227	APARAPGDPQLPVMVFPFGGAFIVGAASSYEGSDLAAREKVLVFLQHLRIGIFGLSTDD	286
QY	206	SHARGNWGLLQMAALRWQENIAAFGDDPQNVTLFQOSAGAMISGLMWSPLASGLFHR	265
DB	287	SHARGNWGLLQMAALRWQENIAAFGDDPQNVTLFQOSAGAMISGLMWSPLASGLFHR	346
QY	266	ALSQSGTALFRLIFITSNPKVAKVAHLAGCNHNSTOILVNCRLALSGTKVMVSNKMF	325
DB	347	ALSQSGTALFRLIFITSNPKVAKVAHLAGCNHNSTOILVNCRLALSGTKVMVSNKMF	406
QY	326	LQNLNFORPELILMSVSDGVVIPPDDPLVLTQGVSSVPYLLGVNNLEFNWLLPYIM	385
DB	407	LQNLNFORPELILMSVSDGVVIPPDDPLVLTQGVSSVPYLLGVNNLEFNWLLPY--	464
QY	386	KPFLNQRMRKETITKMLWSTRLNLTKEQVPLVVEEYLDNVNEHDWKLNRNMDIVQ	445
DB	465	-----NITKEQVPLVVEEYLDNVNEHDWKLNRNMDIVQ	499
QY	446	DATFYATLQTAHVHRD	462
DB	500	DATFYATLQTAHVHRE	516

RESULT 4
 US-09-978-697-254
 ; Sequence 254, Application US/09978697
 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C27
 ; CURRENT APPLICATION NUMBER: US/09/978,697
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29

Query Match 65.1%; Score 2026.5; DB 9; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY 6 LPSTVLPSSLPTAGAGSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLOGKQVH 65
DB 47 LGSTSTPATTSPSSGFGTGLFGSPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQVH 106

QY 66 VGTKPIQVFLGVFSPRPPLGILRFPAPPEPPPEPWKIGIRDTATYPPG----- 110
DB 107 VGTKPIQVFLGVFSPRPPLGILRFPAPPEPPPEPWKIGIRDTATYPPGWSLALSGNSAVARS 166

QY 111 -----CLOESWGLASWYVSTERYKWLRFSEDCLYLVNY 145
DB 167 RLTAATSASRVQASLLPQPLSVWGVYRCLQESWGLASWYVSTERYKWLRFSEDCLYLVNY 226

QY	146	APARPGDPOLPVMMWFFPGAFIVGAASSYEGSDLAAREKVVVLFQHRLGIFGFLSTDD	205	PRIOR APPLICATION NUMBER: 60/077450
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Db	227	APARPGDPOLPVMMWFFPGAFIVGAASSYEGSDLAAREKVVVLFQHRLGIFGFLSTDD	286	PRIOR APPLICATION NUMBER: 60/077632
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QY	206	SHARGNWGLDDQAAALRWQENIAAFGGDPGNVTLFGOSAGAMSTISGLMSPSLASGLFHR	265	PRIOR APPLICATION NUMBER: 60/077641
				PRIOR FILING DATE: 1998-03-11
Db	287	SHARGNWGLDDQAAALRWQENIAAFGGDPGNVTLFGOSAGAMSTISGLMSPSLASGLFHR	346	PRIOR APPLICATION NUMBER: 60/077649
				PRIOR FILING DATE: 1998-03-11
QY	266	AISQSTALFRLFITSNPLKVAKVAHLACGNHNSQTLLVNCRLSALSTKVMRVSNKMRP	325	PRIOR APPLICATION NUMBER: 60/077791
				PRIOR FILING DATE: 1998-03-12
Db	347	AISQSTALFRLFITSNPLKVAKVAHLACGNHNSQTLLVNCRLSALSTKVMRVSNKMRP	406	PRIOR APPLICATION NUMBER: 60/078004
				PRIOR FILING DATE: 1998-03-13
QY	326	LQINFORDEEIIWNSPVPVGDWIPDDPLVLLTGKYSVPYLLGVNNLFNNLLPYIM	385	PRIOR APPLICATION NUMBER: 60/078886
				PRIOR FILING DATE: 1998-03-20
Db	407	LQINFORDEEIIWNSPVPVGDWIPDDPLVLLTGKYSVPYLLGVNNLFNNLLPY--	464	PRIOR APPLICATION NUMBER: 60/078936
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QY	386	KPFLNEQAMRKETITKMLNSTTLNITKEQVPLVVEEYLDNVNEHDMQLNRMMDIVQ	445	PRIOR APPLICATION NUMBER: 60/078910
				PRIOR FILING DATE: 1998-03-20
Db	465	-----NITKEQVPLVVEEYLDNVNEHDMQLNRMMDIVQ	499	PRIOR APPLICATION NUMBER: 60/078939
				PRIOR FILING DATE: 1998-03-20
QY	446	DATFVYATLQTAHYHRD 462		PRIOR APPLICATION NUMBER: 60/079294
				PRIOR FILING DATE: 1998-03-25
Db	500	DATFVYATLQTAHYHRE 516		PRIOR APPLICATION NUMBER: 60/079656
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				PRIOR FILING DATE: 1997-11-21

RESULT 5

US-09-978-192A-254

: Sequence 254, Application US/09978192A

: Patent No. US20020177553A1

: GENERAL INFORMATION:

: APPLICANT: Ashkenazi, Avi

: APPLICANT: Baker Kevin P.

: APPLICANT: Botstein, David

: APPLICANT: Desnoyers, Luc

: APPLICANT: Eaton, Dan

: APPLICANT: Ferrara, Napoleon

: APPLICANT: Filvaroff, Ellen

: APPLICANT: Fong, Sherman

: APPLICANT: Gao, Wei-Qiang

: APPLICANT: Gerber, Hanspeter

: APPLICANT: Gerritsen, Mary E.

: APPLICANT: Goddard, Audrey

: APPLICANT: Godowski, Paul J.

: APPLICANT: Grimaldi, J. Christopher

: APPLICANT: Gurney, Austin L.

: APPLICANT: Hillan, Kenneth J.

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: APPLICANT: Kuo, Sophia S.

: APPLICANT: Napier, Mary A.

: APPLICANT: Pan, James

: APPLICANT: Paoni, Nicholas F.

; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
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; PRIOR APPLICATION NUMBER: 60/082568
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR APPLICATION NUMBER: 60/085697
Query Match 65.1%; Score 2026.5; DB 9; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;
QY 6 LPSTVLPSSLPTAGAGMSMRWILCWSLTLCLMAQTALGALHTKRPQVVKYGTIGLQKQMH 65
Db 47 LGSTSTPATTAPSSTGCTGLFGSKPATGFTLGGTNTGALHTKRPQVVKYGTIGLQKQMH 106
QY 66 VGKTPIQVFLGVFPSPPLGLIRFAPPEPPPPWGIKIDATITPPG----- 110
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QY 111 -----CQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 145
Db 167 RLTAATSASRVOASLLPQLSVWGYRCQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226
QY 146 APARAPGDPQLPVMVFPFGAFIVGAASSYEGSDLAAREKVVLPLOHRLGIFGLSTDD 205
Db 227 APARAPGDPQLPVMVFPFGAFIVGAASSYEGSDLAAREKVVLPLOHRLGIFGLSTDD 286
QY 206 SHARGNWGLDQMAALRWQENIAAFGGDPGNVTLFGOSAGANGISGLMWSPLASGLFHR 265
Db 287 SHARGNWGLDQMAALRWQENIAAFGGDPGNVTLFGOSAGANGISGLMWSPLASGLFHR 346
QY 266 AISQSGTALFRLFITSNPLKVAKVVAHLGACNHNSTQLVNLCLRALSGTKMYRVSNKVRF 325
Db 347 AISQSGTALFRLFITSNPLKVAKVVAHLGACNHNSTQLVNLCLRALSGTKMYRVSNKVRF 406
QY 326 LQNFQRPDEIIWMSFVVDGWIIPDDPLVLLTQCKVSSVYPYLLGVNNLEFNWLLPYIM 385
Db 407 LQNFQRPDEIIWMSFVVDGWIIPDDPLVLLTQCKVSSVYPYLLGVNNLEFNWLLPY-- 464
QY 386 KPFLNRQAMKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKLNRNMDIVQ 445
Db 465 -----NITKEQVPLVVEEYLDNVNEHDWKLNRNMDIVQ 499
QY 446 DATFYATLQTAHYRD 462
Db 500 DATFYATLQTAHYRE 516
RESULT 6
US-09-999-832A-254
; Sequence 254, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Hillan, Kenneth J.
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/0622250
PRIOR FILING DATE: 1997-10-17
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 9; Length 545;
 Best Local Similarity 80.3%; Pred. No. 3.6e-185;
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY	6	LPSTVLPSPLLPTAGAGWMSRWILCWSLTCLMAQALGALHTRKPOVTKYGTLOGKQVH	65
DB	47	LGSTSTPATSAPSSGFGTGLFGSKPATGFTTGGTNGALHTRKPOVTKYGTLOGKQVH	106
QY	66	VGKTPIQVLGVFFSPPLGLLEFAPPEPEPWKGRDATTYPPG-----	110
DB	107	VGKTPIQVLGVFFSPPLGLLEFAPPEPEPWKGRDATTYPPGWSLALSPGWSAVARS	166
QY	111	-----CLOSNGOLASMYSTRERYKWLRFSDCLYLVNY	145
DB	167	RUTATGASRVQASLLPQLPUSVMGYRCLQSGWSGOLASMYSTRERYKWLRFSDCLYLVNY	226
QY	146	APARAGDPQLPVMWFFPGAFVGAASSVEGSDLAAREKVLVFLQHLGIFGFLSTDD	205
DB	227	APARAGDPQLPVMWFFPGAFVGAASSVEGSDLAAREKVLVFLQHLGIFGFLSTDD	286
QY	206	SHARGNWGLLDQMAALRWQENTAAFGDPGNVTLFGQSAGAMISGLMWSPLASGLFHR	265
DB	287	SHARGNWGLLDQMAALRWQENTAAFGDPGNVTLFGQSAGAMISGLMWSPLASGLFHR	346
QY	266	AISQSGTALFRLFITSNPLKAVKVAHLACGHNHSTQILVNCRLALSGTKWVRVSNKMF	325
DB	347	AISQSGTALFRLFITSNPLKAVKVAHLACGHNHSTQILVNCRLALSGTKWVRVSNKMF	406
QY	326	LQNFORDPPEIITWMSPPVGVVIPPDDLVLTLTGKVSVPYLLGVNNLEFNWLLPYIM	385
DB	407	LQNFORDPPEIITWMSPPVGVVIPPDDLVLTLTGKVSVPYLLGVNNLEFNWLLPY--	464
QY	386	KFLNRCQMRKEITKMLNSTRLILNITKEQVPLVVEEYLDNNEHDKMLNRNMDIVQ	445
DB	465	-----NITKEQVPLVVEEYLDNNEHDKMLNRNMDIVQ	499
QY	446	DATEFVYATLQTAHYHRE	462

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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;
 Best Local Similarity 80.3%; Pred. No. 3.6e-185;
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

Oy	6	LPSTVLPSLLPTAGAGSMRWILCWSLTLCLMAQTALGALHTKRPQVTKYGTLOGKQXH	65
		:	
Db	47	LGSTSTPATTSAPSSGFGTGLFQSKATGTTGGTNGALHTKRPQVTKYGTLOGKQXH	106
		:	
Oy	66	VGKTPIQVFLGVFPSPPLGILRFAPPEPPEPWKGIKRDATTYPPG	110
		:	
Db	107	VGKTPIQVFLGVFPSPPLGILRFAPPEPPEPWKGIKRDATTYPPGWSLALSPGWSAVERS	166
		:	
Oy	111	-----CLQBSWGQLASMYSTRERYKWLRFSEDCLYNVY	145

Query Match 65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185; Indels 67; Gaps 2;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;
QY 6 LPSTVLPSSLPTAGACGMRWILCWSLTLCLMAQTALGALHTKRPQVTKYGTLOGKQMH 65
DB 47 LGSTSPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVTKYGTLOGKQMH 106
QY 66 VGTPTQVFLGVDPFSPDPIGLRFAPEPPEPWKGRDATTTPPG----- 110
DB 107 VGKTPQVFLGVDPFSPDPIGLRFAPEPPEPWKGRDATTTPPGWSLALSPGWSAVARS 166
QY 111 -----CLQBSWGQLASMYVSTRERYKWLRFSEDCLYLNVY 145
DB 167 RLATASASRVQASLLPQLSVWGYRCLQBSWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226
QY 146 APAPAGDPOLPVMWFFGGAFIVGAASSYEGSDLAAREKVVLFQHLRIGIFGLSTDD 205
DB 227 APAPAGDPOLPVMWFFGGAFIVGAASSYEGSDLAAREKVVLFQHLRIGIFGLSTDD 286
QY 206 SHARGNWGLDDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSI SGLMMSPLASGLFHR 265
DB 287 SHARGNWGLDDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSI SGLMMSPLASGLFHR 346
QY 266 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 325
DB 347 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 406
QY 326 LQINFORDEEIIWMSPPVVDGWIIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385
DB 407 LQINFORDEEIIWMSPPVVDGWIIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464
QY 386 KPFLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNHDWKLNRNMDIVQ 445
DB 465 -----NITKEQVPLVVEEYLDNVNHDWKLNRNMDIVQ 499
QY 446 DATFYATLQTAHYHRD 462
DB 500 DATFYATLQTAHYHRE 516

RESULT 9
US-09-978-585A-254
; Sequence 254, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

DB 167 RLATASASRVQASLLPQLSVWGYRCLQBSWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226
QY 146 APAPAGDPOLPVMWFFGGAFIVGAASSYEGSDLAAREKVVLFQHLRIGIFGLSTDD 205
DB 227 APAPAGDPOLPVMWFFGGAFIVGAASSYEGSDLAAREKVVLFQHLRIGIFGLSTDD 286
QY 206 SHARGNWGLDDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSI SGLMMSPLASGLFHR 265
DB 287 SHARGNWGLDDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSI SGLMMSPLASGLFHR 346
QY 266 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 325
DB 347 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 406
QY 326 LQINFORDEEIIWMSPPVVDGWIIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385
DB 407 LQINFORDEEIIWMSPPVVDGWIIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464
QY 386 KPFLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNHDWKLNRNMDIVQ 445
DB 465 -----NITKEQVPLVVEEYLDNVNHDWKLNRNMDIVQ 499
QY 446 DATFYATLQTAHYHRD 462
DB 500 DATFYATLQTAHYHRE 516

RESULT 8
US-09-978-608A-254
; Sequence 254, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978.608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 254
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-254

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 254
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-254

Query Match          65.1%  Score 2026.5;  DB 10;  Length 545;
Best Local Similarity 80.3%;  Pred. No. 3.6e-185;
Matches 399;  Conservative 5;  Mismatches 26;  Indels 67;  Gaps 2;

QY 6 LPSTVLSLLPTAGAGSMRWILCWSLTLCLMAQTALGALHTKRPQVTKYGTLOGKQMH 65
DB 6 LGSTSTPATTSAPSSGFGTGLPGSKPATGFTLGGTNTGALHTKRPQVTKYGTLOGKQMH 106
QY 66 VGTPIQVFLGVPSRPPGLILFAPPEPEPKGIRDAITTPPG----- 110
DB 107 VGTPIQVFLGVPSRPPGLILFAPPEPEPKGIRDAITTPPGWSLSPGWSAVARS 166
QY 111 -----CLQBSWGQLASMYVSTREYKWLRFSEDCLYLVNY 145
DB 167 RLATSASRVQASILLPQLSWMGYRCQLQBSWGQLASMYVSTREYKWLRFSEDCLYLVNY 226
QY 146 APARAFGDPQLPVMWPPGAFVGAASSYEGSDLAAREKVLVFLQHLRIGFGLSTDD 205
DB 227 APARAFGDPQLPVMWPPGAFVGAASSYEGSDLAAREKVLVFLQHLRIGFGLSTDD 286
QY 206 SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 265
DB 287 SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346
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DB 347 AISQSGTALFRPLITSNPLKVAKVLAHLAGCNHNSQILVNCCLRALSGTKVNRVSNKWRP 406
QY 326 LQINFORDEEIIWNSPVVDGVPVDDPLVLTQCKVSSVYLLGVNLEPNWLLPYIM 385
DB 407 LQINFORDEEIIWNSPVVDGVPVDDPLVLTQCKVSSVYLLGVNLEPNWLLPY-- 464
QY 386 KFLNDAQVRKETITKMLWSTRLNLITKEQVPLVVEEYLDNVNHDHDKMLRNRMWDIVQ 445
DB 465 -----NITKEQVPLVVEEYLDNVNHDHDKMLRNRMWDIVQ 499
QY 446 DATEVYATLOTAYHRD 462
DB 500 DATEVYATLOTAYHRE 516

RESULT 10
US-09-978-191A-254
; Sequence 254, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;

Best Local Similarity 80.3%; Pred. No. 3.6e-185;

Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

Qy	6	LPSTVLPSPLLPTAGAGMSRWILCWSLTLCLMAQTALGALHTRKRPQVTVKYGLQGQMH	65
Db	47	LGSTSTPATTSAFSSGGTGLFGSKPATGTGLGTNTGALHTRKRPQVTVKYGLQGQMH	106
Qy	66	VGKTPIQVFLGVFPSPRPLGILRAPPEPPEPWKIGIRDATYPPG	110
Db	107	VGKTPIQVFLGVFPSPRPLGILRAPPEPPEPWKIGIRDATYPPGWSLALSPGWSAVARS	166
Qy	111	-----CQBSWGOLASMYVSTRERYKWLRTSEDCLYLNRY	145
Db	167	RLTATSASRVOASLLPOPLSVWGYRCLQESWGOLASMYVSTRERYKWLRTSEDCLYLNRY	226
Qy	146	APARAPGDPQLPVVMWPPGGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGFLSTDD	205
Db	227	APARAPGDPQLPVVMWPPGGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGFLSTDD	286
Qy	206	SHARGNWGLLDQMAALEWVOENIAFGDPCNVTFLQCSAGAMSI SGLMMSPLASGLFHR	265
Db	287	SHARGNWGLLDQMAALRWQENIAFGDPCNVTFLQCSAGAMSI SGLMMSPLASGLFHR	346
Qy	266	AISQSGTALFRLFITSNPLKVAKVAHLACGNHNSTQILVNCRLALSGTKVMRYSNRMRF	325
Db	347	AISQSGTALFRLFITSNPLKVAKVAHLACGNHNSTQILVNCRLALSGTKVMRYSNRMRF	406
Qy	326	LQALNFQDDPBEI IWSMSPVVDGVIPDDPLVLLTQGVKSVVPLLGVNNLEFWLLPYIM	385
Db	407	LQALNFQDDPBEI IWSMSPVVDGVIPDDPLVLLTQGVKSVVPLLGVNNLEFWLLPY--	464
Qy	386	KFPLNRQAMRKETITKMLWSTRTLLNTTKEQVPLVVEEYLDNVNHDWKMLRNRMDIVQ	445
Db	465	-----NITKEQVPLVVEEYLDNVNHDWKMLRNRMDIVQ	499

QY 446 DATFVYATLOTAYHRD 462
Db 500 DATFVYATLOTAYHRE 516

RESULT 11

US-09-978-403A-254
; Sequence 254, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

Qy 6 LPSTVLPSSLPTAGAGMSWILCWSLTLCLMAQTALGALHTKRPQVWTKYGTLOGKQWH 65
Db 47 LGSTSPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVWTKYGTLOGKQWH 106
Qy 66 VGKTPIQVFLGVPSRPPLGILRFAPPEPPKRGIRDAATTYPGWSLALSPGSAVARS 110

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Db 107 VGKTPIQVFLGVPSRPPLGILRFAPPEPPKRGIRDAATTYPGWSLALSPGSAVARS 166
Qy 111 -----CLOESWGOLASMYVSTRERYKWLRESEDCLYLNVY 145
Db 167 RLTSASRYQASLLPOPLSVMGYRCLOESWGOLASMYVSTRERYKWLRESEDCLYLNVY 226
Qy 146 APARAPGDPOLPVVMWPPGGAFIVGAASSYEGSDLAAREKXVLVFLQHRLLGIFGFLSTDD 205
Db 227 APARAPGDPOLPVVMWPPGGAFIVGAASSYEGSDLAAREKXVLVFLQHRLLGIFGFLSTDD 286
Qy 206 SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFQOSAGAMSISGLMMSPLASGLFHR 265
Db 287 SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFQOSAGAMSISGLMMSPLASGLFHR 346
Qy 266 AISOSGTALFRLFTTSNPLKVAKKVAHLAGNNHSTOILVNCJRALSGTKVMRVSNKORF 325
Db 347 AISOSGTALFRLFTTSNPLKVAKKVAHLAGNNHSTOILVNCJRALSGTKVMRVSNKORF 406
Qy 326 LQNLNFORDPBEEIWSMSPVVDGVVIPPDPVLVLTQGVKSVVPYLLGVNNLEFNWLLPYIM 385
Db 407 LQNLNFORDPBEEIWSMSPVVDGVVIPPDPVLVLTQGVKSVVPYLLGVNNLEFNWLLPY-- 464
Qy 386 KPFLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDKMLRNRMDIVQ 445
Db 465 -----NITKEQVPLVVEEYLDNVNEHDKMLRNRMDIVQ 499
Qy 446 DATEFYATLOTAYHRD 462
Db 500 DATEFYATLOTAYHRE 516

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RESULT 12

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US-09-978-564A-254
; Sequence 254, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrata, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

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[illegible]

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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;

Best Local Similarity 80.3%; Pred. No. 3.6e-185; Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY 6 LPTVLPSLLPTAGAGWNRWILCSLTLCLMAQTALGALHTKRPQVVTKYGTLOGKQMH 65
DB 47 LGSTSTPATTSAPSSGFGGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMH 106
QY 66 VGTKPTQVFLGVFFSRPPLGIIRFAPPEPEPWKGIROATTYPPG----- 110
DB 107 VGTKPTQVFLGVFFSRPPLGIIRFAPPEPEPWKGIROATTYPPGWSLALSPGWSAVARS 166
QY 111 -----CLQESWQOLASMYVSTRERYKWLRFSEDCLYLNVY 145
DB 167 RLATASASRVQASLLPQPLSVMGVYRCLOESWQOLASMYVSTRERYKWLRFSEDCLYLNVY 226
QY 146 APARAPDQPLPMWFFPGAFIVGASSYEGSDLAAREKVVLFQHRLGIFGFLSTDD 205
DB 227 APARAPDQPLPMWFFPGAFIVGASSYEGSDLAAREKVVLFQHRLGIFGFLSTDD 286
QY 206 SHARGNWGLDQWALRWVQENIAAFGGDPGNVTLFGSAGAMSTISGLMSPASGLFHR 265
DB 287 SHARGNWGLDQWALRWVQENIAAFGGDPGNVTLFGSAGAMSTISGLMSPASGLFHR 346
QY 266 AISQGTALFRFITSNPKVAKKVAHLAGCHNHNSTQILLVNCRLSALSGTKWVRVSNKGRF 325
DB 347 AISQGTALFRFITSNPKVAKKVAHLAGCHNHNSTQILLVNCRLSALSGTKWVRVSNKGRF 406
QY 326 LQINFORDEEIIWNSPVVDGVVIPPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385
DB 407 LQINFORDEEIIWNSPVVDGVVIPPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464
QY 386 KPELNQAMRKETITKMLNSTRTLLNITKEQVPLVVEEYLDNVNHDWKLNRKMDIVQ 445
DB 465 -----NITKEQVPLVVEEYLDNVNHDWKLNRKMDIVQ 499
QY 446 DATEFVYATLQTAHYHRD 462
DB 500 DATEFVYATLQTAHYHRE 516

RESULT 13

US-09-999-833A-254
; Sequence 254, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Askenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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 ; PRIOR FILING DATE: 1998-04-15
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 ; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/084414
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;

Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

Qy	6	LPSTVLPSLLPTAGAGWSMRWILCWSLTLCLMAQTALGALHTKRPQVTKYGTLOGKQMH	65
Db	47	LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGCTNTGALHTKRPQVTKYGTLOGKQMH	106
Qy	66	VGKTPIQVFLGVPPSRPPLGILRPAPEPPEPWKIGIRDATTYPPG	110
Db	107	VGKTPIQVFLGVPPSRPPLGILRPAPEPPEPWKIGIRDATTYPPGWSLALSFGWSAVARS	166
Qy	111	-----CLOESWGOLASMYSTERYKWLRFSDCLYLVY	145
Db	167	RLTATSASRVQASLLLPQLSVWGYRCLQESWGOLASMYSTERYKWLRFSDCLYLVY	226
Qy	146	APARAPGDPQLPVMWFPFGAFIVGAASYEGSDLAAREKVVLVFIQHLRGI FGLSTDD	205
Db	227	APARAPGDPQLPVMWFPFGAFIVGAASYEGSDLAAREKVVLVFIQHLRGI FGLSTDD	286
Qy	206	SHARGNWGLLDQVAALRWYQENIAAFGGDPGNVTLFGQSAGAWSISGLNWSPLASGLFHR	265
Db	287	SHARGNWGLLDQVAALRWYQENIAAFGGDPGNVTLFGQSAGAWSISGLNWSPLASGLFHR	346
Qy	266	AISQSGTALFRFITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGTKVMRVSNKMR	325
Db	347	AISQSGTALFRFITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGTKVMRVSNKMR	406
Qy	326	LQINFORDEEIIWNSPVDGVIPDDPLVLTQKQSSVSEYLLGVANNLENNLLPYIM	385
Db	407	LQINFORDEEIIWNSPVDGVIPDDPLVLTQKQSSVSEYLLGVANNLENNLLPYIM	464
Qy	386	KPPLNQRMRKETITQVLWSTRTLLNITKEQVPLVVEYLDNVNBDWKLNRNMDIVQ	445

Db 465 -----NITKEQVPLVVEYLDVNEHDWKMLRNMMDIVQ 499
QY 446 DATEVYATLOTAYHRD 462
Db 500 DATEVYATLOTAYHRE 516
RESULT 14
US-09-981-915A-254
; Sequence 254, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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 ; PRIOR APPLICATION NUMBER: 60/085580
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 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;
 Best Local Similarity 80.3%; Pred. No. 3.6e-185;
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;
 6 LPSTVPLSLPAGAGWSNWLCLWSLTLCLMAOTFALCALHTKRPQVVTYKGTGLOKQMH 65
 47 LOSTSTPATTSPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTYKGTGLOKQMH 106

QY 66 VGKTPIQVFLGVFPFSRPPLGILREAPPPEPEPWKGI RDTATTPPG----- 110
 Db 107 VGKTPIQVFLGVFPFSRPPLGILREAPPPEPEPWKGI RDTATTPPGWSLALSPGWSAVARS 166
 QY 111 -----CLQESWGQLASMYVSTRERYKWLRFSDCLYLNYY 145
 Db 167 RL TATSASRVQASLLPQPLSVMGYRCLQESWGQLASMYVSTRERYKWLRFSDCLYLNYY 226
 QY 146 APARAPGDPQLPVMWFFPGGAFIVGAASYEGSDLAAREKVVLFQHLRLGIFGFLSTDD 205
 Db 227 APARAPGDPQLPVMWFFPGGAFIVGAASYEGSDLAAREKVVLFQHLRLGIFGFLSTDD 286
 QY 206 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSISGLMMSPLASGLFHR 265
 Db 287 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSISGLMMSPLASGLFHR 346
 QY 266 AISQSGTALFRIFITSNPLKVAHVLAAGCHNHTQILVNCRLALSGTKVVRVSNKVRF 325
 Db 347 AISQSGTALFRIFITSNPLKVAHVLAAGCHNHTQILVNCRLALSGTKVVRVSNKVRF 406
 QY 326 LQINFORDEEIIWMSPVVDGWIIPDDPLVLTQGVSSVPYLLGVNNLEFNWLLPYIM 385
 Db 407 LQINFORDEEIIWMSPVVDGWIIPDDPLVLTQGVSSVPYLLGVNNLEFNWLLPY-- 464
 QY 386 KFPLNQAVRKETITKMLMSTRTLLNITKEQVPLVVEYLDNVNHDWMLRNRMMDIVQ 445
 Db 465 -----NITKEQVPLVVEYLDNVNHDWMLRNRMMDIVQ 499
 QY 446 DATFVYATLQTAHYHRD 462
 Db 500 DATFVYATLQTAHYHRE 516

RESULT 15
 US-09-978-824-254
 ; Sequence 254, Application US/09978824
 ; Publication No. US2003035216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC14
 ; CURRENT APPLICATION NUMBER: US/09/978,824
 ; PRIOR FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250

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6	PRIOR FILING DATE: 1998-04-15
7	PRIOR APPLICATION NUMBER: 60/081952
8	PRIOR FILING DATE: 1998-04-15
9	PRIOR APPLICATION NUMBER: 60/081838
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13	PRIOR APPLICATION NUMBER: 60/082569
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17	PRIOR APPLICATION NUMBER: 60/082804
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19	PRIOR APPLICATION NUMBER: 60/082700
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24	PRIOR FILING DATE: 1998-04-23
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46	PRIOR FILING DATE: 1998-04-29
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48	PRIOR FILING DATE: 1998-04-30
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Thu Aug 12 09:48:52 2004

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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY      6 LPSTVLPSPPTAGAGWNRWILCWSLTLCLMAQTALCALHTKRPQVVTYKGTLOGKMH 65
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
47 LGSTSTPATSPSGSGFGTGLGSKPATGFTLGGTNTGALHTKRPQVVTYKGTLOGKMH 106
QY      66 VGKTPIQVFLGVFPFRPPLGILRFAPPEPPEPWKGIKRDATTYPG----- 110
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
107 VGKTPIQVFLGVFPFRPPLGILRFAPPEPPEPWKGIKRDATTYPGWSLALSPGWSAVARS 166
QY      111 -----CLESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 145
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
167 RLATTSASRVOASLLPQLPSLVWGYCQLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226
QY      146 APARAPGDPQLPMVWFPFGAFIVGAASYEGSDLAAREKVVLFLOHRLGIFGFLSTDD 205
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY      206 SHARGNWGLLDQWALRWQENIAAFGGDPGNVTLFGOSAGAMSTISGLMSPLASGLFHR 265
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
287 SHARGNWGLLDQWALRWQENIAAFGGDPGNVTLFGOSAGAMSTISGLMSPLASGLFHR 346
QY      266 AISQGTALFRLFTSNPLKVAHVLAHLAGCNHNSTQILVNCRLALSGTKWVSNKWRP 325
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347 AISQGTALFRLFTSNPLKVAHVLAHLAGCNHNSTQILVNCRLALSGTKWVSNKWRP 406
QY      326 LQNFORDPEEIIWMSPPVVDGWIIPDDPLVLLTQCKVSSVPYLLGVANNLEFNWLLPYIM 385
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
407 LQNFORDPEEIIWMSPPVVDGWIIPDDPLVLLTQCKVSSVPYLLGVANNLEFNWLLPY-- 464
QY      386 KFPFLNQAMRKETITKMLASTRLNITKEQVPLVVEEYLDNVNHDWMLNRNMWDIVQ 445
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
465 -----NITKEQVPLVVEEYLDNVNHDWMLNRNMWDIVQ 499
QY      446 DATFVYATLQTAHYHRD 462
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
500 DATFVYATLQTAHYHRE 516
```

Search completed: August 3, 2004, 22:34:11
Job time : 52 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: August 3, 2004, 22:25:31 : Search time 21 Seconds

(without alignments)
2675.041 Million cell updates/sec

Title: US-10-001-227-2

Perfect score: 3112

Sequence: 1 MFSTVLPSTVLSLPTAGA.....KMAFWMSLYQSQRPEKQRF 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:*

2: pir1:*

3: pir2:*

4: pir3:*

5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1290.5	41.5	557	2 A47162	thiolesterase B (E
2	1254	40.3	565	2 S10367	carboxylesterase
3	1251	40.2	567	1 A41010	carboxylesterase
4	1239.5	39.8	566	2 S19307	carboxylesterase
5	1205.5	38.7	561	2 JC2447	carboxylesterase
6	1205.5	38.7	562	2 A55281	carboxylesterase
7	1187.5	38.2	561	2 S71597	carboxylesterase
8	1184.5	38.1	561	2 S62788	carboxylesterase
9	1159.5	37.3	549	2 JX0054	carboxylesterase
10	1149	36.9	540	2 A31584	carboxylesterase
11	1141.5	36.7	554	2 A39060	carboxylesterase
12	1133	36.4	539	2 A29323	carboxylesterase
13	1083	34.8	559	1 JC5308	carboxylesterase
14	1060	34.1	561	2 S47855	carboxylesterase
15	1034	33.2	554	1 S34607	carboxylesterase
16	993	31.9	532	2 A34329	60K esterase (EC 3
17	787	25.3	614	2 A39256	acetylcholinestera
18	761.5	24.5	614	2 JH0314	acetylcholinestera
19	751.5	24.1	614	2 JH0811	acetylcholinestera
20	741	23.8	584	2 S48724	acetylcholinestera
21	740.5	23.8	583	2 S10712	acetylcholinestera
22	727	23.4	612	2 A34967	sterol esterase (E
23	726	23.3	599	2 A57701	sterol esterase (E
24	725.5	23.3	596	1 ACRYE	acetylcholinestera
25	722	23.2	597	2 A33658	sterol esterase (E
26	713.5	22.9	599	1 A38868	acetylcholinestera
27	712.5	22.9	602	1 ACHU	cholinesterase (EC
28	702	22.6	745	2 S13586	triacylglycerol li
29	691	22.2	603	2 S70849	cholinesterase (EC

30 572 21.6 620 2 A54413 acetylcholinestera
31 685.5 21.4 581 2 C39768 cholinesterase (EC
32 653.5 21.0 489 2 B69680 para-nitrobenzyl e
33 653 21.0 664 2 JC7990 acetylcholinestera
34 651.5 20.9 506 2 H75522 triacylglycerol li
35 640 20.6 593 1 S25062 triacylglycerol li
36 620.5 19.9 540 2 S51043 carboxylesterase
37 604 19.4 637 2 S66236 carboxylesterase
38 601.5 19.3 767 2 S47639 acetylcholinestera
39 590 19.0 691 2 JE0150 acetylcholinestera
40 580.5 18.7 578 2 F89068 protein t28C12.4b
41 580.5 18.7 658 2 T32053 hypothetical prote
42 579 18.6 540 2 A75250 carboxylesterase
43 579 18.6 602 2 T37254 acetylcholinestera
44 578.5 18.6 745 2 A25363 acetylcholinestera
45 568.5 18.3 502 2 AE0666 probable esterase

ALIGNMENTS

RESULT 1

A47162

thiolesterase B (EC 3.-.-.-) precursor - mallard

C:Species: Anas platyrhynchos (mallard)

C:Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 18-Jun-1999

C:Accession: A47162

R:HWang, C.S.; Kolattukudy, P.E.

J. Biol. Chem. 268, 14278-14284, 1993

A:Title: Molecular cloning and sequencing of thioesterase B cDNA and stimulation of exp

A:Reference number: A47162; NUID:93300823; PMID:8314791

A:Accession: A47162

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-557 <HWA>

A:Cross-references: GB:L05493; NID:G213100; PIDN:AAA49223.1; PID:G213101

A:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: hydrolase

F:56-545/Domain: cholinesterase homology <CH>

Query Match 41.5%; Score 1290.5; DB 2; Length 557;
Best Local Similarity 46.0%; Pred. No. 1.4e-96;
Matches 260; Conservative 106; Mismatches 172; Indels 27; Gaps 11;

QY 27 ILCSLTCLMAQTALGALHTKRPQVTKYGTLOGQKHV--GKTPQVFLGVFPSPPL 84
Db 8 LLSLTILTAGITAVATGQ-KAEQPEVNTYGSVGYQVKNAASRVNVLGLPFAKPPV 66
QY 85 GILRFAPPEPPEPKGIRDTATTPPGCLQES-WGQLASMYVSTRERYKWLRFSDCLYLN 143
Db 67 GLRFSEPPPEPKGVRDAASYPMLQDVKLQY:SDAITNKEKVRQLGISDCLYLN 126
QY 144 VYAPARAPGDPQLPVMVWFGCAFIVGAASYESGDLAAREKVVVLVFLQHRLGFGLST 203
Db 127 VVTPVSTBEQKLPVFMVHGGGLVSGAASVYDGSALAAFDNVVVTITQVRLGIAGVFS 186
QY 204 DDSHARGNGWGLDQWALRWYQENIAAFGDPGNVTLFGOSAGAMSISGLMMSPLASGLF 263
Db 187 GDKARGNGWGLDQWALRWYQENIAAFGDPGNVTLFGOSAGAMSISGLMMSPLASGLF 246
QY 264 HRAISQSQTALFRLFITSNPLKVAKVAHLACGNHNSQTILVNCRLASGTGKVMRVSNKM 323
Db 247 HKAISESCTAV-RILFTQEPEEQARIAAAAGCEKSSAALVECLREKTEAEMEQITLKM 305
QY 324 RFLQNFORDDEEIIWMSPVVDGVIPDDPLVLLTQGVSSVYLLGVNNLEFNWLLPY 383
Db 306 -----PPMFI---SASLDGVFPFKSPRLSEKVINAVPYIIGVNNCFEGWILPR 352
QY 384 IMKPELNFQAMRKETITKMLWSTRL--LNTKQVPLVVEYLDNVNEHDKMLNRMM 441
Db 353 MKKPEFTEGEEKVARQVQLSTLALSKGAFSDIVLVNEYI-GVAENR-AQVRDGLL 410
QY 442 DIVQDQTFVYATLOTAHYHRDAGLPVLYIEFEHH---ARGIIVKPRTDGADHGDMEYPLF 498

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Db      411  DSTDPLFVSVAEVAHHRDAGNPVYFEFQHRPSSAGV--PEFVKADHADIAPV 468
Qy      499  GGFATGLSGKGEKALSLQMKYKWNANFATGNPDGNLPCWRPNKDEKYLQDFTTRVG 558
Db      469  GKPLFAGNATEEBAKLSRTVMKWTNFAFNGNPNPGEGLVFWPQYDMDEYLEIDLTQKAA 528
Qy      559  MKLKEKKVAFWMSLYQSOREKQO 583
Db      529  KKLKKEKQEFWMLTQOIMSDRRK 553

RESULT 2
S10367
carboxylesterase (EC 3.1.1.1) ES-10 precursor, microsomal - rat
N:Alternate names: hydrolase A
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
C/Accession: S10367; S12468; S51202; S23460; S14361
R:Robbi, M.; Beaufay, H.; Octave, J.N.
Biochem. J. 269, 451-458, 1990
A:Title: Nucleotide sequence of cDNA coding for rat liver pi 6.1 esterase (ES-10), a car
A:Reference number: S10367; MUID:90351366; PMID:2386485
A:Accession: S10367
A:Molecule type: mRNA
A:Residues: 1-565 <ROB1>
A:Cross-references: EMBL:X51974
A:Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found
A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 5 in having 265-Lys
R:Robbi, M.
submitted to the EMBL Data Library, February 1990
A:Reference number: S12468
A:Accession: S12468
A:Molecule type: mRNA
A:Residues: 1-264, 'K', 266-565 <ROB2>
A:Cross-references: EMBL:X51974; NID:956898; PIDN:CAA36236.1; PID:956899
R:Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Biochem. Biophys. 315, 495-512, 1994
A:Title: Purification and characterization of two rat liver microsomal carboxylesterases
A:Reference number: S51202; MUID:95077430; PMID:7986098
A:Accession: S51202
A:Molecule type: protein
A:Residues: 1-48 <WOR>
R:Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A:Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting t
A:Reference number: S23460; MUID:92299008; PMID:1606962
A:Accession: S23460
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-185, 'O', 187-422, 'M', 424-505, 'N', 507-565 <WED>
A:Cross-references: EMBL:X65266; NID:957553; PIDN:CAA46391.1; PID:957554
R:Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
Biochem. J. 274, 693-697, 1991
A:Title: Purification and characterization of carboxylesterases from rat lung.
A:Reference number: S14361; MUID:91190080; PMID:2012599
A:Accession: S14361
A:Molecule type: protein
A:Residues: 13-26, 'D', 28-37 <GAU>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-565/Product: carboxylesterase #status predicted <MAT>
F:50-551/Domain: cholinesterase homology <CHE>
F:79-489/Binding site: carboxylate (Asn) (covalent) #status predicted
F:221,466/Active site: Ser, His #status predicted

Query Match      40.3%  Score 1254; DB 2; Length 565;
Best Local Similarity 42.8%  Pred. No. 1.3e-93;
Matches 240; Conservative 120; Mismatches 183; Indels 18; Gaps 6;

Qy      28  LKNSLTLCMAQTALG-----ALHTRKQVWTKYGTLOGKQMHVGTPIQVFLGVPFSR 81
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      6  LVM---LFLAACTAWGYPSPFPVVNTVKGVKLVKNLEGAQ-----PVAVFLGIPPAK 57
Qy      82  PPLGILPAPPEPEPKGIGRDATITPPGGLQES-WGLASMYVSTRYKWLRFSDCL 140
Db      58  PPLGSLFAPQPAEPWNFVKNTITSYPPMCSQAVGQVLSELFTRKENIPILQFSDCL 117
Qy      141  YLNVYAFARAPGPQPLPMVMVFFPGGAFIVGAASVEGSDLAAREKVVVLVFLQRLGIFG 200
Db      118  YLNVYTPADLTQKSRLPVMVHIHGGGLVVGASTYDQVLSAHENVVVTIQVRLGIWGF 177
Qy      201  LSTDDSHARGNWGLLDQAAALRWQENIAAFGDPGNVILFGOSAGAMSISGLMMSPLAS 260
Db      178  FSTGDESRGNWGLDQVAALHWQDNIAFNGNPGSVTFIGSAGGFSVSALVLSPLAK 237
Qy      261  GLPHRAISQSGTALFRLFITSNPLKVAKVVAHLAGCNHNSQLVNLCLRALSGTKVRVS 320
Db      238  NLPHRAISESGVLTSLALITTDSPKPIANLIATLSGCKTTTSAMVHCLRQKTEDELETS 297
Qy      321  NKMRFLQINFORPEEIIWMSMPVVDGVIPTDPLVLLTQGVSSVPYLLGVNNEFNL 380
Db      298  LKLNLFKLDLLGNPKESYPLPTVIDQVLPKTPPEILAEKSFNTVPYIVGINKQFPGMI 357
Qy      381  LPYIMKEPLNARQMRKETITKMLWSTRTLLNITKSOVLVVEYLDNVNEHDMWLNRNM 440
Db      358  IPTLMGYPLSEGKLDQKTAKSLKWSYPTLKISERKIPVVAEKYFGTD--DPAKERDLP 415
Qy      441  MDIVQDATFYVATLQTAHYHRDAGLPVLYVEFHHARGI-IVKPRTDGADHGDVYFLFG 499
Db      416  QDLVADVIFGVPSVMVSRSHRDAGATPMYEFYRPSFVSAMRPKTVIGDHGDELFSVFG 475
Qy      500  GPFATGLSGKGEKALSLQMKYKWNANFATGNPDGNLPCWRPNKDEKYLQDFTTRVGM 559
Db      476  SPFLKDGASBEETNLSKQVMKYWANFARNGSPNGGLPHWPEYDQKEGVLKIGASTQAAQ 535
Qy      560  KLKEKKVAFWMSLYQSOREPK 580
Db      536  RLKDKEVAFWSELRAKEAAEE 556

RESULT 3
A41010
carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage [validated] - human
N:Alternate names: carboxylesterase, hepatic; monocyte/macrophage serine esterase
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C/Accession: A41010; JH0327; A47376; A49816; P02802; I61085; A48809; I57004
R:Murger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J. Biol. Chem. 266, 18832-18838, 1991
A:Title: A serine esterase released by human alveolar macrophages is closely related to
A:Reference number: A41010; MUID:92011649; PMID:1918003
A:Accession: A41010
A:Molecule type: mRNA
A:Residues: 1-567 <MON>
A:Cross-references: GB:M73499; NID:9179927; PIDN:AAA5649.1; PID:9179928
A:Note: parts of this sequence, including the amino end of the mature protein, were conf
R:Long, R.M.; Calabrese, M.R.; Martin, B.M.; Pohl, L.R.
Life Sci. 48, PL43-PL49, 1991
A:Title: Cloning and sequencing of a human liver carboxylesterase isoenzyme.
A:Reference number: JH0327; MUID:91148424; PMID:1997784
A:Accession: JH0327
A:Molecule type: mRNA
A:Residues: 61-567 <LON>
A:Cross-references: GB:M55509; NID:9179929; PIDN:AAA35650.1; PID:9179930
R:Shibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.
Genomics 17, 76-82, 1993
A:Title: Molecular cloning and characterization of a human carboxylesterase gene.
A:Reference number: A47376; MUID:94010913; PMID:8406473
A:Accession: A47376
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA; DNA
A:Residues: 1-3, 'PALV', 8-11, 'A', 13-567 <SHI>
A:Cross-references: GB:D21088; NID:9455476; PIDN:BA04650.1; PID:9458470
A:Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correspond

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R:Zschunke, F.; Salmassi, A.; Kreipe, H.; Buck, F.; Parwaresch, M.R.; Radzun, H.J.
Blood 78, 506-512, 1991
A:Title: cDNA cloning and characterization of human monocyte/macrophage serine esterase
A:Reference number: A49816; MUID:91300111; PMID:2070086
A:Accession: A49816
A:Molecule type: mRNA
A:Residues: 'G', 65-185, 'G', 187-361, 363-567 <ZSC>
A:Cross-references: GB:X52973; NID:G36421; PIDN:CAA37147.1; PID:G1335304
R:Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
Gene 108, 289-292, 1991
A:Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.
A:Reference number: F80280; MUID:92084150; PMID:1748313
A:Accession: F80280
A:Molecule type: mRNA
A:Residues: 114, 'H', 116-280, 'A', 282-300, 'IGNSYLTYRETREST', 318-336, 'R', 338-382, 'GSP', 383-400
A:Cross-references: GB:M65261; NID:G187028; PIDN:AAA83932.1; PID:G187029
A:Experimental source: liver
A:Note: differences between this sequence and other reports appear to be due to frameshift
R:Kroetz, D.L.; McBride, O.W.; Gonzalez, F.J.
Biochemistry 32, 11606-11617, 1993
A:Title: Glycosylation-dependent activity of baculovirus-expressed human liver carboxylesterase
A:Reference number: A48809; MUID:94032283; PMID:8218228
A:Accession: I61085
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-55, 'G', 57-361, 363-535, 'G', 537-567 <KRO1>
A:Cross-references: GB:L07765; NID:G180949; PIDN:AAA35711.1; PID:G180950
A:Accession: A48809
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-17, 'A', 18-55, 'G', 57-535, 'G', 537-567 <KRO2>
A:Cross-references: GB:L07764; NID:G180947; PIDN:AAA16036.1; PID:G180948
C:Genetics:
A:Gene: GDB:CES1; HMSC
A:Cross-references: GDB:1128044; OMIM:114835
A:Map position: 16q13-16q22.1
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; liver
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-145/Domain: propeptide #status predicted <PRO>
F:50-553/Domain: cholinesterase homology <CHE>
F:146-567/Product: carboxylesterase #status experimental <MAT>
F:564-567/Region: endoplasmic reticulum retention signal #status atypical
F:221,468/Active site: Ser, His #status predicted

Query Match 40.2%; Score 1251; DB 1; Length 567;
Best Local Similarity 44.2%; Pred. No. 2.3e-33;
Matches 250; Conservative 111; Mismatches 192; Indels 12; Gaps 9;
QY 26 WILCWSLTLCLMAQTALGALHTKRPQVY-TKYGTLQCK--QMHVGKTPICVFLGVFPSP 82
DB 2 WLRATILA-TLSAAG--HPSPPPVVDVHGKVLGKFLVSLGFAQPAIFLGIPIPAK 58
QY 83 PLGILRAPPEPPKGIKIRDTATYPPGCLQIE-SWGLASMYVSTRERYKWLRFSDCLY 141
DB 59 PLGLRPTPPQAPSPFVKNATSYPMCTQDPKACQLSELFTNKENIPLKLSDCILY 118
QY 142 LNVYAPARAGDPQLPVMWVFGGAFIVGAASVEGSDLAAREKVLVFLQHLRIGIFGL 201
DB 119 LNIYTPADLTKKRLLPVMWVHGGGLVGNASTYDGLAAAHENVVVTIQRLLGWFF 178
QY 202 STDDSHARGNGLLDQMAALRWYQENIAAFPGDPGNVTLFGOSAGAMISGLMMSPLAS 261
DB 179 STGDESRGNWGLDQVAALRWYQDNIAFGGNGSVTI-FGESAGGESVSVLVSLPLAKN 238
QY 262 LFHRAISQSCTALFRFLITSNPLK-VAKKVAHLACGNHSTQILVNCIRALSGTKMVRVS 320
DB 239 LFHRAISESSVALTSVLVKGVDKPLAEQIATAGCKTTISAVVHCLQKTEBELLETT 298
QY 321 NKMRFLQNFQRPDEEIIWMSPPVVDGWIIPDDPLVLLTQCKVSSVPYLLGVNNLEFNWL 380
DB 299 LKMKFLSLDQGPRESPLGLTVIDGMILLKTFEELQAEARNFHTVPVYVGVINKQEFGL 358

Query Match 39.8%; Score 1239.5; DB 2; Length 566;
Best Local Similarity 44.2%; Pred. No. 2e-92;
Matches 248; Conservative 110; Mismatches 192; Indels 11; Gaps 7;
QY 26 WILCWSLTLCLMAQTALGALHTKRPQVY-TKYGTLQCKQMHVG--KTIQVFLGVFPSP 82
DB 2 WLL--PIVLTSLASATWAGOPAPFPVDTAQRVGLKYVSLGLELAQPAVFLGVFPAPK 59
QY 83 PLGILRAPPEPPKGIKIRDTATYPPGCLQIESWQ--LASMYVSTRERYKWLRFSDCL 140
DB 60 PLGLRFPAPPQAPSPFVKNATSYPMCCQDPVVEQWTSDFLTNGKRLT-LFESDCL 118
QY 141 LNVYAPARAGDPQLPVMWVFGGAFIVGAASVEGSDLAAREKVLVFLQHLRIGIFG 200
DB 119 LNIYTPADLTKKRLLPVMWVHGGGLVGNASTYDGLAAAHENVVVTIQRLLGWFF 178
QY 201 STDDSHARGNGLLDQMAALRWYQENIAAFPGDPGNVTLFGOSAGAMISGLMMSPLAS 260
DB 179 STGDESRGNWGLDQVAALRWYQENIAFGGDPGSGVTIFGESAGGESVSVLVSLPLAK 238
QY 261 GLFHRATISQSCTALFRFLITSNPLKVAKKVAHLACGNHSTQILVNCIRALSGTKMVRVS 320
DB 239 NLFHRAISESSVALTSVALVRKMKAAKQIAVLGCKTTTSVAVFVHCLQKSEDELLD 298
QY 321 NKMRFLQNFQRPDEEIIWMSPPVVDGWIIPDDPLVLLTQCKVSSVPYLLGVNNLEFNWL 380
DB 299 LKMKFLSLDQGPRESPLGLTVIDGMILLKTFEELQAEARNFHTVPVYVGVINKQEFGL 358
QY 381 LPYTKFPLNRQAMRKETITKMLWSTRLTNITKEQVPLVVEEYLDNVNBNHDKMLNRM 440

Db 359 LPTMGFPSEGLDKDQKATSLWKSYPANIPDELTPVATDKYLGDDDPVKK--KDLF 416
QY 441 MDIVQDQATFYATQTAHYHRDAGLVLYLYFEHH--ARGIIIVKPRDTGADGDEMYFLFG 499
Db 417 LDLMGDVVEGVPSTVARQHRDAGATYMYEQYRPSFSSDKPKTKVIGDHGDEIFSVFG 476
QY 500 GPATGLSGMGEKALSQMKMYWANFARTGNPDNGNLPWPRYNKDEKYLQDFTTRVGM 559
Db 477 FPLKGDAPPEEVSLSKTKWKFANFARSGNPNGBGLPHMPYDQBEGLYQGVNTQAAK 536
QY 560 KLKEKMAFWMSLYQSORPEK 580
Db 537 RLKGEVAFWNDLLSKEAKK 557

RESULT 5

JC2447
carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JC2447; S23462
R:Robbi, M.; Beaufay, H.
Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994
A:Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGASYN).
A:Reference number: JC2447; MUID:95032008; PMID:7945287
A:Accession: JC2447
A:Molecule type: mRNA
A:Residues: 1-561 <ROB>
A:Cross-references: GB:X81395; NID:G550146; PIDN:CAA57158.1; PID:G550147
A:Experimental source: liver
R:Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A:Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting
A:Reference number: S23460; MUID:92299008; PMID:1606962
A:Accession: S23462
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 503-554, 'R', 556-561 <MED>
A:Cross-references: EMBL:X65295; NID:G57557; PIDN:CAA46390.1; PID:G57558
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-561/Product: carboxylesterase ES-3 #status predicted <SIG>
F:50-551/Domain: cholinesterase homology <CHE>
F:79,107,489/Binding site: carbohydrate (Asn)
F:221,466/Active site: Ser, His #status predicted

Query Match 38.7%; Score 1205.5; DB 2; Length 561;
Best Local Similarity 43.3%; Pred. No. 1.1e-89;
Matches 238; Conservative 114; Mismatches 191; Indels 7; Gaps 6;
QY 28 LC-MSLTLCLMAQTALGALHTKRPQVVTYKGTGKQGMHV-GKT-PIQVFLGVFPRPEL 84
Db 1 MCLVALILVLAFTAGGHPSSLPVDTLQKVLGKVSLEGFTQPVAVFLGVFAKPEL 60
QY 85 GILRFAPPEPEPKGRDATTTPPGCLQES-WGOLASMYVSTRYKWLRESEDCLYLN 143
Db 61 GSLRFAPQPAEPMSFVNTSYPPMCSQDPVAGQIVNDLLTNWENISLQFSEDCLYLN 120
QY 144 VYAPARAPGDPOLPVMWVFPFGAFIVGAASVYSGSDIAAREKVVVFLQRLGIFGLST 203
Db 121 IYTPADLTKRDLRFPMWIHGGGLVLGASTYDGLALSTHENVVVVIQVRLGIWGFEST 180
QY 204 DDSHARGNGLLDQMAALRWQENIAAFPGDPGNVTLFGQSAGAMSISGLMWPLASGLF 263
Db 181 GDESRGNWGLHDQVAALHWQDNIIDNFGDPGPGSVTFPGESAGGESVSLVLSPLAKNLF 240
QY 264 HRAISQSQTALFRLFITSNPLKVAKKVAHLACGNHNSQTQLVNCRLALSCTKVMVSNQM 323
Db 241 HKALISEGVALTAGLVKNTFPLAEKIAVSGCKSTTSASWVHCLAQKTEEBELLETTLK 300
QY 324 RFLQNFQRPDEEIIWSNMSPVVDGVIPTDDPLVLLTOGKVSVPVLLGVNNEFNLPLPY 383

Db 301 NLFSLDLHGDSRQSPVPVTLVDGVVLPKMPEILAEKDFNTVPYIVGINKQEFGWILFT 360
QY 384 IMKFPPLNRQMRKETITTKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDKMLRNRHMDI 443
Db 361 MMNYPSPDKLDPMATATSLKSSFLNLNUPPEEAPVAVSEKYLRHTDDPDRN--KDQLLSL 418
QY 444 VQDATFYATQTAHYHRDAGLVLYLYFEHH--ARGIIIVKPRDTGADGDEMYFLFGGPF 502
Db 419 IGVIFGVPSVIVSRGHRDAGARTYMYEQYRPSFSSKMKPSFVVGHDGDEIVSFGALI 478
QY 503 ATGLSMGKALKSLQMKMYWANFARTGNPDNGNLPWPRYNKDEKYLQDFTTRVGMKLC 562
Db 479 LRGGTSKEEINLSKMMKFWANFARNGPNNGOGLPHMPEYDQKEGYLQIGATTQQAOKLR 538
QY 563 EKKMAFWMSL 572
Db 539 EXEVAFWSEL 548

RESULT 6

A55281
carboxylesterase (EC 3.1.1.1) egasyn - mouse
N:Alterate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-
C:Species: Mus musculus (house mouse)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
C:Accession: A55281
R:Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.;
Genomics 11, 956-967, 1991
A:Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-
A:Reference number: A55281; MUID:92147141; PMID:1783403
A:Accession: A55281
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-562 <OVN>
A:Cross-references: GB:S80191; NID:G244727; PIDN:AAB21335.1; PID:G244728
A:Note: sequence extracted from NCBI backbone (NCBIN:80191, NCBI:P:80194)
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum
F:51-552/Domain: cholinesterase homology <CHE>
F:222,467/Active site: Ser, His #status predicted

Query Match 38.7%; Score 1205.5; DB 2; Length 562;
Best Local Similarity 42.4%; Pred. No. 1.1e-89;
Matches 241; Conservative 119; Mismatches 188; Indels 21; Gaps 9;
QY 28 LCWS-LTLCLMAQTALGALHTKRPQVVTYKGTGKQGMHVK-----TPIQVFLGV 78
Db 1 MCLVALILVLAFTAGGHPSSPPMV---DTVQGVKYL--GKYISLEGFTQPVAVFLGV 55
QY 79 FSRPLGLTRFAPPEPEPKGRDATTTPPGCLQES-WGOLASMYVSTRYKWLRFSE 137
Db 56 FAKPLGSLRFPAPQPAEPMSVNTSYPPMCSQDPVAGQIVNDLLTNKKEIPLQFSE 115
QY 138 DCLYLVNYPARAPGDPOLPVMWVFPFGAFIVGAASVYSGSDIAAREKVVVFLQRLGI 197
Db 116 DCLYLVNYPADLTKRDLRFPMWIHGGGLVLGASTYDGLVLTSHENVVVVIQVRLGI 175
QY 198 PGFLSTDSDSHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMWSP 257
Db 176 WGFSTGDEHGRGNWGLHDQVAALHWQDNIIDNFGDPGPGSVTFPGESAGGESVSLVLS 235
QY 258 LASGLFHRASQSQTALFRLFITSNPLKVAKKVAHLACGNHNSQTQLVNCRLALSCTKVM 317
Db 236 LAKNLFQRAISESGVALTAGLVKNTFPLAEKIAVSGCKNTTSAAMVHCLRQKTEEBEL 295
QY 318 RVSNKORFLQNFQRPDEEIIWSNMSPVVDGVIPTDDPLVLLTOGKVSVPVLLGVNNEF 377
Db 296 GTTLKLNLFKLDLHGDSRQSPVPVTLVDGVVLPKMPEILAEKDFNTVPYIVGINKQEF 355
QY 378 NWLLPYIMKFPPLNRQMRKETITTKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDKML 436
Db 356 GWILPTMWNYPSPDKLDPMATATSLKSSFLNLNUPPEEAPVAVSEKYLRHTDDPDRN--RD 412

Qy	437	RNEMMDIVODATEVTVATLCTAHYHRDAGLPVLYEFEPHH-ARGIIVPRTDGDAGHDEMY	495
Db	413	KDOLLELIGBVGVPGVPSIVSRGHRDAGATMYTFYQSPFSSEMKPDPVTWVGCHGEIY	472
Qy	496	FLFGGPFATGLSGXGKEKALSLOMKYXWAFNARTGNPNNDGNLPCWPRYNKCEKYLQLDFTT	555
Db	473	SVEGAPILRGSTSEEBEINLSXMMKFWANFARNGNPNFGQLPAWPEIDQKEGYLQIGATT	532
Qy	556	RVGMKULKEKKMAFWMSLY-QSORPEKQKQ	583
Db	533	QQAQKLKEKEVAFWTELLAKQLPTEHTE	561

RESULT 7

S71597
carboxylesterase (EC 3.1.1.1) precursor, liver - rat

N:Alternate names: hydrolase C

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998

C:Accession: S71597

R:Yan, B.; Yang, D.; Parkinson, A.
Arch. Biochem. Biophys. 317, 222-234, 1995

A:Title: Cloning and expression of hydrolase C, a member of the rat carboxylesterase family

A:Reference number: S71597; MUID:95177656; PMID:7872788

A:Accession: S71597

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-561 <YAN>

A:Experimental source: liver; endoplasmic reticulum

C:Function:

A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-561/Product: carboxylesterase #status predicted <MAN>

F:50-551/Domain: cholinesterase homology <CHE>

F:558-561/Region: endoplasmic reticulum retention signal

F:79,301/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:221,466/Active site: Ser, His #status predicted

Query Match	38.2%	Score 1187.5	DB 2	Length 561
Best Local Similarity	41.1%	Pred. No. 3.2e-88		
Matches 230	Conservative 123	Mismatches 196	Indels 11	Gaps 5

Qy 24 MRWILCWSLITCLMA--QTALGAIHTKRPQVVTKYGTLOQMVKTKPTIQVLGVPFSSR 81
 :
 :
 :
Dd 3 LRSLFLVSLATCVVCNPNSSPPVDTMKGKLVGYASLEGVTSVA---VFLGVVFPAK 57
 :
 :
 :
 :

Qy 82' PPILIRAPPEPPPEPWKGIARDATYPGCLQESW-GQLASMYVSTRYKWLRISEDCI 140
|||||
|||:::
Dd 58 PPGSLRAPPQPAEPWSVKNTTTPPMCSQDATKGORNDDLNRKEKVHLOFSEDCI 117
|||||
|||:::

QY 141 YLNVYA^PARAPGDPQLPVMWFPGGAFIVGAASSVEGSDLAAREKVVLFLOHRIIGFV 200
|||:||| :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Dd 118 YLNIYTPADFTKDSRMPVMWIHGGLTGGASTVDGRVLSAYENVVVAIQRLGIWGF 177

QY	201	LSTDDSHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMTSIGLWMSPLAS	260
		: : : : : : : : : : :	
Db	178	FSTGDEHGRGNWGHLDOVAALHWQDNIANFGDPSVTIFGESAGGSVSVLVLSPLSK	237

QY 261 GLFHRAISQSGTALFRLFTSNPLKVAKKVAHLACGNHNSTQILVNCRLALSCTKMVRVS 320
: : : : : : : : : : : : : : : : : : :
Db 238 NLYHRAISESGVVLTQTFTKDVPAAKOIADMACGKTTSATIIVCHLROKTEELLEIM 297

Qy 321 NKMFLQLNFQRDEEIIKWSMSPVVDGVIPDDPLVLTTQGVSSVPYLLGNNLEFNWL 380
|| :|: ||| :|: | |:| :|: ||| :|: | |:| :|: ||| :|: | |:| :|: ||| :|: |
Dd 298 EXANLIKUSSORTKESYHFLSTVIDDVLPKPDKIELAEKNFNTVPYIVGINKECGWL 357

QY 381 LPYIMKFPINRQAMRKETITKMLWSTRITLNI7KEQVPLVVEEYLDNVNEHDKWMLNRNM 440

Db 358 LPTMMRFVDPVKLDKKAIMLEKFASTYGIPEDIIPVAIEKY -RKGSDDPTKIRDGI 415

Qy	441	MDIVQDAIFVATLTQATSHYHBDAGLVPYLVEFEHH-ARGIIIVPRTDGDAGHDEMVFELRG	499
Db	416	LAFIGDVLFCIPSVMSVRDRRDAGAPTVIYEQIYPSFSQPKOVGVGDHADVVSFVG	475
Qy	500	GFATGLSGKGEKALSLQMKYKWNANFARTGNPDGNLPCWPRYKNKBEKYLQDLDTTRVGM	559
Db	476	APILRDGASEEBEIKLSKVMKMFANFARNGNPNARGLPHWPQDYDQKEEYLQIGATTQQSQ	535
Qy	560	KLUKKKMAFMSLYQSQPE	579
Db	536	RLKABEAVFWTOLLAKROFO	555

RESULT 8

S62788
carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat
N:Alternate names: hydrolase B
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: S62788; S51203; A55304; S49257
R:Robbi, M.; van Schaftingen, E.; Beaufay, H.
Biochem. J. 313, 821-826, 1996
A:Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal palmitoyl)
A:Reference number: S62788; MUID:96190723; PMID:8611161
A:Accession: S62788
A:Molecule type: mRNA
A:Residues: 1-561 <ROB>
A:Cross-references: EMBL:X81825; NID:G550417; PID:G550418
A:Experimental source: liver
R:Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Biochem. Biophys. 315, 495-512, 1994
A:Title: Purification and characterization of two rat liver microsomal carboxylesterase
A:Reference number: S51202; MUID:95077430; PMID:7986098
A:Accession: S51203
A:Molecule type: protein
A:Residues: 19-48 <WOR>
A:Experimental source: liver
R:Yan, B.; Yang, D.; Brady, M.; Parkinson, A.
J. Biol. Chem. 269, 29688-29696, 1994
A:Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and r
A:Reference number: A55304; MUID:95050819; PMID:7961958
A:Accession: A55304
A:Molecule type: mRNA
A:Residues: 1-6, 'F', 8-59, 'P', 61-212, 'A', 214-252, 'T', 254-309, 'IT', 312-341, 'N', 343-424, 'F',
A:Cross-references: GB:U0697; NID:G562007
A:Note: the sequence in GenBank entry RNU10697, release 107, (PID:G562008) has the codon
R:Robbi, M.; Beaufay, H.
submitted to the EMBL Data Library, September 1994
A:Reference number: S49257
A:Accession: S49257

A;Cross-references: EMBL:X81825; NID:g550417; PIDN:CAA57419.1; PID:g550418

C:Function:
A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-561/Product: carboxylesterase SS-4 #status experimental <VAT>
F:50-551/Domain: cholinesterase homology <CHE>
F:221,466/Active site: Ser, His #status predicted
F:301/Binding site: carbohydrate (Asn) #status predicted

Query Match	38.1%	Score 1184.5	DB 2	Length 561
Best Local Similarity	41.7%	Pred. No. 5.6e-88		
Matches 234	Conservative 123	Mismatches 131	Indels 13	Gaps 7

Qy	24	MRWILCWSLTLCMLM--AQTALGALHTKRPQVVTXYGTLOGQMHWGKTPTQVFGLGVPSFR81
Db	3	LSFLIYLSLATCWVGNPNSSPPVVDDTTTGKVLGYVSLEGVTSQA-----VFLGVPFAPK57

QY 82 PPLGILRFAPPEPPWKGIRDATTYPGCLQE-SWQLASMYVSTRERYKWLFSEDCI 140

Db 58 PFLGSLRFAAPQPAEPWSEVFNKNTTTPWCSODAAKQRMNDLLTNREKIHLEFSEDC 117
 Qy 141 YLVYIPARAPGDPQLPVMWFFGGGAFIVGAASSYEGSLAAREKVVLFVLOHRLGIFG 200
 Db 118 YLNIYTPADFTKSRSLPVMWVIHGGGTLGGASTYDGRVLSAYENVVVVAIQYRLGIFG 177
 Qy 201 LSTDDSHARGNWGLLDMAALRWVQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLAS 260
 Db 178 PSTGDEHSRGNWAHLDOAALRWVQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLAS 237
 Qy 261 GLPHRAISQGTALFLRFTTSNPLKVAKVLAHAGNHNSTQILVNCRLALSGLTKMVRV 320
 Db 238 NLFHRAISESGVFLPGLLTQKVRPAKQIADWAGCETTTSATVCHLRQKTEELLETIM 297
 Qy 321 NKRFQLNFORPDEBIIWMSVPVGVWIPDDPLVLLTGQKVSVPYLLGVNNLEFNW 380
 Db 298 KQNLIKSSQRDNKESYHFLSTVDNVLDPDKPKEILAEKPNVTVPYIVGINKQECGWL 357
 Qy 381 LPYIMKFP-LNROAMRKETITKMLSTRLLNTTKQVPLVVEEYLDNVNEHDKWMLNR 439
 Db 358 LPTWGVFPADVELDKQWALT-LLEKFAISLYGIPEDIIPVAIEKY--RKGSDDSIKIRDG 414
 Qy 440 MMDIVQDATFYATLQTAHYHRDAGLPVLYEPEHH-ARGIIIVKPRTDGADHDEMFLF 498
 Db 415 ILAFIGDVSFSPVMSVSRDHRDAGAPTYMYEYQYPSFSSPPQPKHVVGDDHADDLYVF 474
 Qy 499 GGPFPATGLSMGKALKSLQMKWYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVG 558
 Db 475 GAPTLDGASEEBIKLSKWKWYANFARNNGNPNRGLPHWPQYDQKEEYVLIQATTOQS 534
 Qy 559 MKLKEKMAFMWSLYQSORPE 579
 Db 535 QRLKAEVAFWTLAKRQPO 555

RESULT 9
 JX0054
 Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Aug-1998
 C:Accession: JX0054
 R: Takagi, Y.; Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.
 J. Biochem. 104, 801-806, 1988
 A:Title: Molecular cloning and nucleotide sequence of cDNA of microsomal carboxylesterase
 A:Reference number: JX0054; MUID:89174514; PMID:3235453
 A:Accession: JX0054
 A:Molecule type: mRNA
 A:Residues: 1-549 <TAK>
 A:Experimental source: liver
 A:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; microsome
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-549/Product: carboxylesterase El #status predicted <MAT>
 F:50-538/Domain: cholinesterase homology <CHE>
 F:79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:21,453/Active site: Ser, His #status predicted

Query Match 37.3%; Score 1159.5; DB 2; Length 549;
 Best Local Similarity 42.6%; Pred. No. 5.8e-06;
 Matches 240; Conservative 104; Mismatches 192; Indels 27; Gaps 9;
 Qy 26 WI--LCW-SUTLCIM--AQTALGALHTKRPQVVTYGTLOGKQMHVGKTPIQVFLGVPS 80
 Db 2 WLCLVWASLAVCPWCHGSSPPVDDTKGVLGVVSLGFTQ-----PVAVFLGVPPA 56
 Qy 81 RPLGIILRPAPPPEPPKIRATTPPCLOES--WGQLASMYSTRERYKWLRFSEDC 139
 Db 57 KPPLGLSRFAPPPEPPKIRATTPPCLOES--WGQLASMYSTRERYKWLRFSEDC 116
 Qy 140 LYNVYIPARAPGDPQLPVMWFFGGGAFIVGAASSYEGSLAAREKVVLFVLOHRLGIFG 199
 Db 117 LYLNIYSPADLTNKSRLPVMWVIHGGGTLGGASTYDGRVLSAYENVVVVAIQYRLGIFG 176

Qy 200 FLSTDDSHARGNWGLLDMAALRWVQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLAS 259
 Db 177 LFTSGDEHSRGNWAHLDOAALRWVQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLAS 236
 Qy 260 SGLPHRAISQGTALFLRFTTSNPLKVAKVLAHAGNHNSTQILVNCRLALSGLTKMVRV 319
 Db 237 KNLPHRAISESGVFLPGLLTQKVRPAKQIADWAGCETTTSATVCHLRQKTEELLETIM 297
 Qy 320 NKRFQLNFORPDEBIIWMSVPVGVWIPDDPLVLLTGQKVSVPYLLGVNNLEFNW 379
 Db 288 KTEAELELTVKLDNT---SMSTVIDGVLPKTPBEILTEKSFNTVPYIVGINKQECGWL 343
 Qy 380 LLPYIMKFP-LNROAMRKETITKMLSTRLLNTTKQVPLVVEEYLDNVNEHDKWMLNR 439
 Db 344 IIPTMGNNLLSEGRMNEKMASSFLKRFSPNLNISESVIPAIEKYLRTGDDPAK--KEL 401
 Qy 440 MMDIVQDATFYATLQTAHYHRDAGLPVLYEPEHHARGII-VKPRTDGADHDEMFLF 498
 Db 402 LDMFSDVFFGIPAVLMSRLRDAQAPTYMYEYQYPSFSSPPQPKHVVGDDHADDLYVF 461
 Qy 499 GGPFPATGLSMGKALKSLQMKWYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVG 558
 Db 462 GTPFLKEGASBEETNLKLVKWFANFARNNGNPNRGLPHWPQYDQKEEYVLIQATTOQA 521
 Qy 559 MKLKEKMAFMWSLYQSORPEKQ 581
 Db 522 QRLKAEVAFWTLAKRPPQTE 544

RESULT 10
 A31584
 Carboxylesterase (EC 3.1.1.1) precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 18-Jun-1999
 C:Accession: A31584
 R: Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R.
 Biochem. Biophys. Res. Commun. 156, 866-873, 1988
 A:Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for a multigene family
 A:Reference number: A31584; MUID:89050119; PMID:2973315
 A:Accession: A31584
 A:Molecule type: mRNA
 A:Residues: 1-540 <LON>
 A:Cross-references: GB:M20629; GB:X13587; NID:G203279; PIDN:AAA40871.1; PID:G203280
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:1-9/Domain: signal sequence #status predicted <SIG>
 F:10-540/Product: carboxylesterase #status predicted <MAT>
 F:41-529/Domain: cholinesterase homology <CHE>
 F:70,265,266,293,366,467/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:212,444/Active site: Ser, His #status predicted

Query Match 36.9%; Score 1149; DB 2; Length 540;
 Best Local Similarity 43.8%; Pred. No. 4e-85;
 Matches 237; Conservative 96; Mismatches 188; Indels 20; Gaps 8;
 Qy 46 HTRKRPQV--TKYGTLOGKQMHV-GKT-PIQVFLGVPSRPLGLRFPAPPPEPPKIR 102
 Db 10 HPSSPPVVDVTTKGVLGVVSLGFTQTPVAVFLGVPPAKPPLGSLRFPAPPPEPPKIR 69
 Qy 103 DATYTPPCLOES--WGQLASMYSTRERYKWLRFSEDCLYNVYAPARAGDPQLPVMW 161
 Db 70 NTTTYPMWCSQGVVGVKLLADMLSTGKESIPLEFSEDCLYNLYSPADLTNKSRLPVMW 129
 Qy 182 FPGGAFIVGAASSYEGSLAAREKVVLFVLOHRLGIFG-STDDSHARGNWGLLDQMAAL 221
 Db 130 IHGGGLIIGGASPSYGLSALSAHENVVVVTIYRLFGGLFSTGDEHSRGNWAHLDOAAL 189
 Qy 222 RWQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLASGLFHRALISQGTALFLRFTTS 281
 Db 190 RWQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLASGLFHRALISQGTALFLRFTTS 249
 Qy 282 NPLKVAKVLAHAGNHNSTQILVNCRLALSGLTKMVRVSNRMRFLQLNFORPDEPPIW 341

Db 250 NTOAQAQMIATSGCNNTSSAAMVQCLRQ-----KTEAEELLETVKLDNT-----SM 296
Qy 342 SPVVDGVVDDPLVLLTQGVSSVPYLLGVNLEFNWLLPYINKPLNQARKEITYK 401
Db 297 STVLDGVLLPTEBEILTEKSFNTVPVIVGNKQEFGWIIPTWGNLLSEGRNNEKMAS 356
Qy 402 MLASTRLNITKEQVPLVVEEYLDNVNEHDWMLNRMDIVQDATFVYATQTAHYHR 461
Db 357 FLKRFSPNLNISESVIPIETKYLGRDTPAKK--KELLDDMFSDVFFGIPAVLMSSLR 414
Qy 462 DAGLPVLYFEHARGII-VKPTDGDADGDEMYFLFGGPFATGUSMGKEKALSQMK 520
Db 415 DAGAPTYNYEFQVAPSPVSQRPQTQVGDHGBEIFSFGTFPFKEGASBEETNLSLVNK 474
Qy 521 YWANFARTGNPDGNCPCWPRYNKDEKYLQDFTTRVGMKLKEKMAFWMSLYQSORPEK 580
Db 475 FWANFARGNPNGEGLFHWPKYDQKGYLQIGATTQQAQKLKGEVAFWTELLAKNPQT 534
Qy 581 Q 581
Db 535 E 535

RESULT 11
A39060
carboxylesterase (EC 3.1.1.1) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 18-Jun-1999
C:Accession: A39060
R:Ovnic, M.; Tepperman, K.; Medda, S.; Elliott, R.W.; Stephenson, D.A.; Grant, S.G.; Gar
Genomics 9, 344-354, 1991
A:Title: Characterization of a murine cDNA encoding a member of the carboxylesterase mul
A:Reference number: A39060; MUID:91169540; PMID:1840565
A:Accession: A39060
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-554 <OVN>
A:Cross-references: GB:M57960; NID:G192853; PIDN:AAA63297.1; PID:G192854
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:50-540/domain: cholinesterase homology <CHE>
F:221,455/Active site: Ser, His #status predicted

Query Match 36.7%; Score 1141.5; DB 2; Length 554;
Best Local Similarity 41.5%; Pred. No. 1.7e-84;
Matches 233; Conservative 113; Mismatches 190; Indels 25; Gaps 10;

Qy 26 WI--LW-SLTLCLMAQATL-GALHTKRPQVVTYCTLQGMHVGKTPIQVFLGVPPS 80
Db 2 WLHALVWASLAVCPILGHSLLPPVDTQGVKLGKISLEGFEQ-----PVAVFLGVPPA 56

Qy 81 RPLGLILRFAPPPPPKGIKIRDTATYPPGCLQES-WGQLASMYVSTREYKWLRFSEDC 139
Db 57 KPFLGLSLRFAPPPQFAEFWSFKVNTATYPPNCSQDAGWAKILSDMFSTEKILFLKISEDC 116

Qy 140 LYLVNVPAPARAPDPPVPMVWPFPGGAFIVGAASSYEGSDLAAREKVLVFLQHRLLGIRG 199
Db 117 LYLVNISPDLTKSSQLPVMWTHGGGLVIGGRSPNGLSAHEENVVVTIYRLGIGW 176

Qy 200 FLSTDOSHARGNGLLDQMAALRWQENTIAAFGDPGNVTLPQSGAGAMSISGLMMSPILA 259
Db 177 LFTSGDEHSPGNWAHLDQLAALRWQDNIAFGNPNDSVTIFGESSGGISVSVLVSLPG 236

Qy 260 SGLFHRALISOGTALFRLFTITSPLKVAHVLAHCNHNSTOILVNCRLALSGIKWMEV 319
Db 237 KDLFHRALISGVVNTNVGKNQIQAENLIATLSQCNNTSAAVQCCURQKTESBELLEI 296

Qy 320 SNKORFLQNLNFORDPDEEIIWMSFPVVDGVVIPPDDPLVLLTQGVSSVPYLLGVNLEFNW 379
Db 297 SGKL--VQYNI-----SLSTMIDGVVLPKAPPEILAEKSFNTVPVIVGNKQEFCK 345

Qy 380 LLPIYINKPLNRQARKEITIKMLMSTRLLNITKEQVPLVVEEYLDNVNEHDWMLNR 439

Db 346 IIPMQLNLLPEGMKNEETASLLRRFHESEINISESMIPAVIEQVLRGVDDPAK--SEL 403
Qy 440 MMDIVQDATFVYATQTAHYHRDAGLPVLYFEHARGIIVK-PRTDGADGDEMYPLF 498
Db 404 ILDMFGDIFFGTIPAVLLSRSLRDAGVSTYMEFFRPSFVSQDKRPQTVEGDHGBEIPFVF 463
Qy 499 GGPFPATGLSMGKEKALSQMKYWANFARTGNPDGNCPCWPRYNKDEKYLQDFTTRVG 558
Db 464 GAPLLKEGASBEETNLSQMKWFWANFARGNPNGEGLFHWPEYDEQGYLQIGATTQQA 523
Qy 559 MKLKEKMAFWMSLYQSORPE 579
Db 524 QRLKAEVAFWTELLAKNPPE 544

RESULT 12
A29923
carboxylesterase (EC 3.1.1.1), TCCD-induced 60K microsomal - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 08-Dec-1988 #sequence_revision 08-Dec-1988 #text_change 21-Aug-1998
C:Accession: A29923; A29471
R:Korza, G.; Ozols, J.
J. Biol. Chem. 263, 3486-3495, 1988
A:Title: Complete covalent structure of 60-kDa esterase isolated from 2,3,7,8-tetrachlo
A:Reference number: A29923; MUID:88139431; PMID:3343253
A:Accession: A29923
A:Molecule type: protein
A:Residues: 1-539 <KOR>
R:Ozols, J.
J. Biol. Chem. 262, 15316-15321, 1987
A:Title: Isolation and characterization of a 60-kilodalton glycoprotein esterase from l
A:Reference number: A29471; MUID:88033124; PMID:3667634
A:Accession: A29471
A:Molecule type: protein
A:Residues: 1-71;193-208;436-446;532-539 <OZO>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein
F:32-526/domain: cholinesterase homology <CHE>
F:61,363/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:195,441/Active site: Ser, His #status experimental

Query Match 36.4%; Score 1133; DB 2; Length 539;
Best Local Similarity 41.3%; Pred. No. 8e-84;
Matches 227; Conservative 115; Mismatches 177; Indels 30; Gaps 10;

Qy 46 HTRKPVVTKYGTLOGKQMHVGR-----TPIQVFLGVPPSPPLGILRFAPPEPEP 97
Db 1 HPSAPPVV---DTVKGKVL--GKTVSLGEGPACPVAVFLGVPPFAKPLGLSLRFAPPPQAES 55

Qy 98 WKGIRDATTYPPGCLQE--SWGQLASMYVSTREYKWLRFSEDCLYLVNVPAPARAPDQ 155
Db 56 WSHVKNNTTSYPPMCCSDAVSGHMLSELTNRKENIP-LKFSEDCLYLVNITPADLTKRGR 114

Qy 156 LPVWVWPFPGGAFIVGAASSYEGSDLAAREKVLVFLQHRLLGIRGIFLSTDSDSHARGNWGL 215
Db 115 LPVWVWTHGGGLWVGASTYDGLSALAHENVVVTIYRLGIGGFGFNIDE-----L 166

Qy 216 DQMAALRWQENTIAAFGDPGNVTLPQSGAGAMSISGLMMSPASGLFHRALISOGTALF 275
Db 167 FLVAVNRWQDNIAFGDPGCVTIFGESAGQSVSILLISPLTKNLFHRAISSEGVALL 226

Qy 276 RLFTITSPLKVAHVLAHCNHNSTOILVNCRLALSGTKVMRYSNKMFQLNLFQDRPE 335
Db 227 SSLFRKNTKSLAEKIALTEAGCKTTTSVAVWVHCLBQKTEBELMEVTLKMKFNALDLVGDPK 286

Qy 336 EIIWMSFPVVDGVVIPPDDPLVLLTQGVSSVPYLLGVNLEFNWLLP-YIMKFPPLNRQAM 394
Db 287 ENTAPLTVIDGVLLPKAPABIEEKKYNMLPYVMVGINQQEFGWIIIPQMLGYPLSEGL 346

Qy 395 RKEITIKMLSTRLLNITKEQVPLVVEEYLDNVNEHDWMLNRMDIVQDATFVYATL 454
Db 347 DQKATELLWKSYPVNVSKELTPVATEKYLGITDDDPVK--KDLFLDMLADLLFGVPSV 404

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QY 455 QTAYHRDAGLPVLYFEFHH-ARGIIVKPRTDGADHGMVFLFGPPATGLSMGKEKA 513
Db 405 NVARHRDAGAPTYMEYRPSFSMDMRPKTVIGDHGEIDFISVGLAPFLKEGATEEETK 464
QY 514 LSLQMKYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGMKLEKKKQVAFWMSLY 573
Db 465 LSKWKYANFARNGNPNNGEGLPQWPAYDKYEGYLQIGATTCAQAKLKDKVAFWTELM 524
QY 574 --OSQREK 580
Db 525 AKBAARPRE 533

RESULT 13
JC5408
carboxylesterase (EC 3.1.1.1) - human
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JC5408
R:Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.
Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A:Title: Molecular cloning and characterization of a novel putative carboxylesterase, p
A:Reference number: JC5408; MUID:97289502; PMID:9144407
A:Accession: JC5408
A:Molecule type: mRNA
A:Residues: 1-559<SCH>
A:Cross-references: GB:Y09616; NID:G2058317; PIDN:CAA70831.1; PID:G2058318
A:Experimental source: intestine
C:Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters
C:Genetics:
A:Gene: GDB:CEB2; iCB; CE2
A:Cross-references: GDB:Y9959011
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:58-544/Domain: cholinesterase homology <CHE>
F:15-95,123-280,291-428/Disulfide bonds: #status predicted
F:111,276/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:228,457/Active site: Ser, His #status predicted

Query Match 34.8%; Score 1083; DB 1; Length 559;
Best Local Similarity 40.8%; Pred. No. 9.6e-80;
Matches 232; Conservative 94; Mismatches 204; Indels 38; Gaps 10;

QY 27 ILCSLTLCLMAQTALGALHTKRPQVVKYGTQKGOMHV--GKTPIQVFLGVFSPRPPL 84
Db 13 VACGLLLLVRGQ---GQDSASPIRTTHTGQVLSLVHVKGANAGVQTFLGIRPAKPP 68
QY 85 GLIRFAPPEPPEPWKGIKRDATTYPPGCLQESWGQASVMYVSTRERYKLRFSDECLYLV 144
Db 69 GPRFAPPEPPEPESWGVROGTHTPMCLQDLTAVESEFLSQFNMTFSPSMSEDCLYLSI 128
QY 145 YAPARPGDPLPVMWFFPGCAFIVGAASVEGSDLAAREKVVFLQHLRGLFGLSTD 204
Db 129 YTPAHSHEGSLNLPVMWVHGGALVFGMASLYDGSMLAALNVVWVVIQYRLGVLFSTG 188
QY 205 DSHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLVMPLASGLPH 264
Db 189 DKHATGNWGLDQVAALRWQENIAFHGGNPDRTVTFGESAGTSVSSLVVSPISGLPH 248
QY 265 RAISQSGTALFRFITSNPLKVAHVLAAGCNHNSTQILVNCRLALSGTKVMYSNQR 324
Db 249 GAINESGVALLPGLIASSADVISVWNLASACQVDSEALVGLCRGKSEELAINKPKF 308
QY 325 FLQNFORDPEEIIWMSFPVWDGVVLPDDPLVLLTGQKVSVPYLLGVNLLPENLLPYI 384
Db 309 MI-----PGVVDGVFLPRHPQVLLASADFPQVPSIVGVNNEFGMLIPKY 353
QY 385 MKPELNQAMRKETITKMLNSTLTLLNITKEQVPLVVVEYL-DNVNEHDKMLRNRMMDI 443
Db 354 MRIYDTQKEMDREASQAALQKMLTLLMPTTFGLDLREEYIGN---GDPQTLQAQFQM 410
QY 444 VQDATFYATLQTAHYHRDAGLPVLYFEFHHARGI-IVKPRTDGADHGMVFL-----F 498

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Db 411 MADSMFVIPALQVAHF-QCSRAPVYFVFOHQPSWLKNIRPPHMKADHGDDELFFVFRSFF 469
QY 499 GGPATGLSMGKEKALSLQMKYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVG 558
Db 470 GGNVIKETE--EBEQLSRKMKYANFARNGNPNNGEGLPHPWLPFDOBEOYLQNLQPAVG 527
QY 559 MKLKEKMAFW-----MSLYQSQRPEKQ 581
Db 528 RALKAHRLQFWKALPKQIQELESPEER 555

RESULT 14
S47655
carboxylesterase (EC 3.1.1.1) precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 20-Jun-2000
C:Accession: S47655
R:Sone, T.; Isobe, M.; Takabatake, E.; Wang, C.-Y.
Biochim. Biophys. Acta 1207, 138-142, 1994
A:Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putative
A:Reference number: S47655; MUID:94318665; PMID:8043605
A:Accession: S47655
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-561<SON>
A:Cross-references: EMBL:D28566; NID:G531238; PIDN:BAA05913.1; PID:G531239
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:58-545/Domain: cholinesterase homology <CHE>
F:227,459/Active site: Ser, His #status predicted

Query Match 34.1%; Score 1060; DB 2; Length 561;
Best Local Similarity 41.1%; Pred. No. 7.1e-78;
Matches 234; Conservative 97; Mismatches 191; Indels 48; Gaps 14;

QY 29 CWSLTLCLMAQTALGALH---TKRPQVVKYGTQKGOMHV--GKTPIQVFLGVFSPRP 83
Db 8 CWRVAVACGLLLLVHVGQDSVSPINHTGTQVRGKLVVYKGVGVVAFGLIPAKPP 67
QY 84 LGILRFAPPEPPEPWKGIKRDATTYPPGCLQESW--GQLASMYVSTRER---YKWLRFSD 138
Db 68 VGLRFAPPEPPEPESWGVROGTHTPMCLQDLTAVESEFLSQFNMTFSPSMSEDCLYLSI 121
QY 139 CLYLVNYPARAPGDPOLPVMWFFPGCAFIVGAASVEGSDLAAREKVVFLQHLRGLF 198
Db 122 CLYLVNITPAHAGHGSNLPVMWVHGGALVNGWASMDGSLAATEDIVISIQYRLGIL 181
QY 199 GFLSTDSDSHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLVMSP 258
Db 182 GFFSTGDEHARGNGLDQVAALRWQENIAFGGDPGNVTLFGVSAGGTSVSSLVSPM 241
QY 259 ASGLFHRARISQSGTALFRFITSNPLKV-AKKVAHLACGNHNSTQILVNCRLALSGTKVM 317
Db 242 SKGLFHGAIMQSGVALLPDLISDTPEAVYTFVWVANOQSGCEAKDSEALVHCLREKTBAIL 301
QY 318 RVSNKMRFLQNFORDPEEIIWMSFP-VWDGVVLPDDPLVLLTGQKVSVPYLLGVNLL 376
Db 302 AINQ-----VFINTPGVVDGIFLPRHPQELLASVDHPHVPESIIIGVDSDE 345
QY 377 FNWLLPYMKPPLNQAMRKETITKMLNSTLTLLNITKEQVPLVVVEYLDNVNEHDKML 436
Db 346 CGWGVPLFMGLDHIKNTITRETLPAFLKRAEHMMLPEPCSDLLMQEYMGDV--EDPQTL 403
QY 437 RNRWMDIVQDATFYATLQTAHYHRDAGLPVLYFEFHHARGI---IVKPRTDGADHGM 493
Db 404 QAQFRELKMDPMFVLPALKVAYFOR-SHAPVYFVFOHQSFINKDKARSHVRADHGDH 462
QY 494 MYFLFGGPPFATGLSMG--KEKALSQMKYANFARTGNPDGNLPCWPRYNKDEKYLQ 550
Db 463 VAFVFGSDF-WGLKIDLITEEKLNRKMKYANFARNGNPNSEGLPYWPELVHDDQYLK 521
QY 551 LDFITRVGMKLEKKKMAFWMSLYQSQRPEK 580

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Db      522 LDIQPAVGRAUKSRKXLFHWTKIL-----PQK 547

RESULT 15
S34607
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S34607
R:Aida, K.; Moore, R.; Negishi, M.
Biochim. Biophys. Acta 1174, 72-74, 1993
A:Title: Cloning and nucleotide sequence of a novel, male-predominant carboxylesterase
A:Reference number: S34607; MUID:93326638; PMID:7916639
A:Accession: S34607
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-554 <AID>
A:Cross-references: GB:S64130; NID:9404388; PIDN:AAB27606.1; PID:G404389
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:46-536/Domain: cholinesterase homology <CHE>
F:215/443/Active site: Ser, His #status predicted

Query Match      33.2%; Score 1034; DB 1; Length 554;
Best local Similarity 41.1%; Pred. No. 9e-76;
Matches 232; Conservative 89; Mismatches 205; Indels 38; Gaps 9;

QY      34 LCIMAGTALGALHTKRPQVVKYGLQGMVHGKTP--IQVFLGVPSRPLGILREAP 91
Db      5  LLIPTTVIGPKVT-QPEVDITPLGRVGRQGVKDTDRMNVNVLGIPFAQPLGRFSA 63
QY      92 PEPEPWKGIKRDATTYPGCGLOESWQGLASMYSTRERYKWLRFSEDCCLYLNVIYAPARAP 151
Db      64 PLPQWEGVURDASINPPMCLQDV-ERMNSRFTLNKMKIIPISDCCLTNIYSPTTEIT 122
QY      152 GDPQLPMVWFFPGAFIVGAASVYEGSDLAAREKVLVFLQHLGIFGELSTDDSHARGN 211
Db      123 AGKRPVWVWIHGSLRVGSSTSHDGSALAAAGDVVVVTVQYRLGIFGELSTGDKHMPGN 182
QY      212 WGLDQWALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRALISQSG 271
Db      183 RGFDDVVAALRWQGNIAAFGGDPNCVTIFGNSAGGIIVSSLLSPMSAGLFHRALISQSG 242
QY      272 TALFRLFTTNPVKVAKVAHLAGCNHNSTQILVNCRLALSGTKVMVRSNKNRFLQLNFQ 331
Db      243 VVISKILEDLNANSEACNFANSVACGSAGFAELVQCLLQKEGKDLITKKNV----- 293
QY      332 RDBEIIWNSPVVDGVVIPPDDPLVLLTQCKVSSVPEYLLGVNNLLENWLLPYIMKPEPLNR 391
Db      294 -----NISYTVNDSFFPQPKULANKQFTVPYLLGVNHEFGWLL---LKEWNIL 342
QY      392 QAMRKETITKMLKSTRLL---NITKEQVPLVVEEYLDNVNHDWMLRNRMMDIVQDAT 448
Db      343 DKMEHLSQEDLLENSRPLLAHQMLPPEIMPTVIDEYLDNGS--DESATRYALQELLGDI 400
QY      449 FVYATLQTAHYHRDAGLPVLYLFEFHARGII-VKPRDGDADGDEMYFLFGGPPATGLS 507
Db      401 LVIPTLIFSXYLQDAGCFVLYEFQHTPPSSFAKFKPAWKADHSSNAFVFGGFFLTDES 460
QY      508 -----MGKEKALSLOMKYANFARTGNPNDGNLPCWPRVYNKDEKYLQDLDTTRVGM 559
Db      461 SLLAFPAATEEEKQLSLTMAQHSQFARTGNPNKGKGLPPWPQLNLEQYLEIGLEPRTGV 520
QY      560 KLEKKVAFWMSLYQSQRPEKQRQ 583
Db      521 KLEKKRLQFWTETLPRIQEWHR 544

Search completed: August 3, 2004, 22:28:52
Job time : 23 secs

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FT CARBOHYD 476 476 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 557 AA; 61637 MW; 03E3D9A037F6B0 CRC64;
Query Match 41.5%; Score 1290.5; DB 1; Length 557;
Best Local Similarity 46.0%; Pred. No. 4.8e-95;
Matches 260; Conservative 106; Mismatches 172; Indels 27; Gaps 11;
QY 27 ILCSLTLCLMAQTALGHTKRPQVTKYCTLOGKQHV--GKTPQVFLGVPRRPPL 84
DB 8 LLSLITAGTALVATQ--RAEQEVVNTGSRVGYQVKNAAERSVNVFLGPFAPKPV 66
QY 85 GILFAPPEPEPWKGIARDATTPPGCLOES--WGQASMYVSTRERYKMLRFSEDCLYLN 143
DB 67 GPLRFSBPQPEPWKGVDRDAASYPMLCQKVLQGVLSDAITNRKEKVRQLQISEDCLYLN 126
QY 144 VYAPARAPGDPQLPVMVWFGGAFIVCAASYSYSGSLAAREKVLVFLQHRIGIFGLST 203
DB 127 VYTPVSTEEQKLPFVFMVHGGGLVSGAASSYDGSALAFDNVVTIQYRLGIAGYFT 186
QY 204 DSHARGNGLDQMAALRWQENIAAFGDPGNVTILFGQAGAMSGISGLMSPLASGLF 263
DB 187 GDXHARGNGLDQMAALRWQENIAAFGDPGNVTILFGQAGAMSGISGLMSPLASGLF 246
QY 264 HRAISQSTALFLRFTSPLKVAKVHAGNHNSTQILLNCLRALSGTKVMRVSNKM 323
DB 247 HKAISEGTAV--RLFTPEQPEEQARIAAAGCEKSSAALVECLREKTEAEMEQTILKM 305
QY 324 RFLQNFQRPDEETIIMSPPWGVVDPDPLVLLTGKVSVPYLLGVNNLEFNWLLPY 383
DB 306 -----PPMFI-----SASLDGVFPKPSROLLSEKVINAVPYIIGVNNCEFGHILPR 352
QY 384 IMKPLNRQMRKETTITKMLWSTRL--LNITKEQVPLVVEEYLDNVNHDHMKLRNKM 441
DB 353 MKRFPPETEGLEKDVARQLQSTLALSFKGAPSDIVDLVYNEYI--GVAENR--AQVRDGLL 410
QY 442 DIVQDAPFVATQTAHYHREDAGLPVLYVEFEHH--ARGIIVKPTDGDHGDHMYFLF 498
DB 411 DSTADPLFVSVEVAVRHHDAGNPVYFVQHRPSSAAGV--PEFVADHADAETAFV 468
QY 499 GGPATGLSKGPKALSLQMKMYANFARTGNPDGNLPCWPRYNKDEKYLQIDETTRVG 558
DB 469 GKPFPLAGNATEEBEAKLSRTVMKYTNFARNGNPGEGLVHPQYDMDERYLBIDLTQKAA 528
QY 559 MKLKEKQWAFMSLYQSQRPEKQO 583
DB 529 KKLKERKMFWMQLTQIMSRRRK 553
RESULT 2
ES10 RAT
ID ES10 RAT STANDARD; PRT; 565 AA.
AC P16303; Q64574;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Liver carboxylesterase 10 precursor (EC 3.1.1.1) (Carboxylesterase ES-10) (PI 6.1 esterase) (ES-HVEL).
DE 10 (PI 6.1 esterase) (ES-HVEL).
CS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Liver;
RX MEDLINE=90351366; PubMed=2386485;
RA Robbi M., Beauchamp H., Octave J.-N.;
RT "Nucleotide sequence of cDNA coding for rat liver pi 6.1 esterase (ES-10), a carboxylesterase located in the lumen of the endoplasmic reticulum.";
RL Biochem. J. 269:451-458(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Liver;

RX MEDLINE=92299008; PubMed=1506962;
RA Medda S., Proia R.L.;
RT "The carboxylesterase family exhibits C-terminal sequence diversity reflecting the presence or absence of endoplasmic-reticulum-retention sequences.";
RL Eur. J. Biochem. 206:801-806(1992).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96130267; PubMed=8541339;
RA Ghosh S., Mallonee D.H., Hylemon P.B., Grogan W.M.;
RT "Molecular cloning and expression of rat hepatic neutral cholesteryl ester hydrolase.";
RL Biochim. Biophys. Acta 1259:305-312(1995).
CC -!- FUNCTION: PROBABLY INVOLVED IN THE METABOLISM OF XENOBIOTICS AND OF NATURAL SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a carboxylic anion.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X51974; CAA3236.1; -;
DR EMBL; X65296; CAA46391.1; -;
DR EMBL; L46791; AAA88507.1; -;
DR HSP; P21836; 1VAA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Glycoprotein; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 565 LIVER CARBOXYLESTERASE 10.
FT ACT_SITE 221 221 BY SIMILARITY.
FT ACT_SITE 353 353 BY SIMILARITY.
FT ACT_SITE 466 466 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 562 565 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 186 186 R -> Q (IN SPRAGUE-DAWLEY).
FT VARIANT 265 265 K -> N (IN SPRAGUE-DAWLEY).
FT VARIANT 423 423 I -> M (IN SPRAGUE-DAWLEY).
FT VARIANT 506 506 S -> N (IN SPRAGUE-DAWLEY).
FT CONFLICT 420 420 A -> E (IN REF. 3).
FT CONFLICT 491 492 SK -> TQ (IN REF. 3).
SQ SEQUENCE 565 AA; 62144 MW; F973AF2A71CC1F84 CRC64;
Query Match 40.5%; Score 1259; DB 1; Length 565;
Best Local Similarity 43.0%; Pred. No. 1.6e-92;
Matches 241; Conservative 120; Mismatches 182; Indels 18; Gaps 6;
QY 28 LCWSLTLCLMAQTALG-----ALHKRPQVTKYCTLOGKQHVCKTPIQVFLGVPR 81
DB 6 LVW---LFAACTAWGYPSPVNTVKGLGKYVNLGFAQ-----EVAFLGIPFAK 57
QY 82 PPLGILRFAPPEPEPWKGIARDATTPPGCLOES--WGQASMYVSTRERYKMLRFSEDC 140
DB 58 PPLGSLRFRAPPQPAEPWNVFVNTTSYPPMCSQDVGQVLSLFTNRKNIFLQFSEDC 117
QY 141 YLNVYAPARAPGDPQLPVMVWFGGAFIVCAASYSYSGSLAAREKVLVFLQHRIGIF 200

Db 118 YLNVYTPADLTNKSRLPVMWIIHGGGLVVGASTYDGOVLSAHENVVVVITQYRLGNGF 177
QY 201 LSTDSDHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFQSGAGAMSISGLMMSPLAS 260
Db 178 FTGDEHSGNWHLDQVAALHWQDNIAFGNPGSVTFGESAGGSFVSALVLSPLAK 237
QY 261 GLFHRAISOGTALPFLFTSINPLKVAKKVAHLACNHNSTOILVNCRLRALSGTKMVRVS 320
Db 238 NLFHRAISESGVVLTSALITDSKPIAKLIATLSGCKTTTSAMVHCLROKTEDELLETS 297
QY 321 NKMRFLQALQFQDPPEIINWSMPVVDGVIIPDPLVLLTQGVSSVPVLLGVNNLENNWL 380
Db 298 LKLNLEKLLGNPKESYFPLFTVIDGVLPKTPPEILAEKSFNVPIVIGINKPEFGWI 357
QY 381 LPYIMKPPNLRQAMRKETITKMLWSTRLINLTKEQVPLVBEYLDNVNHEHDKMLNRNM 440
Db 358 IPTLMGYPLSEGKLDQKAKSLKWSYPTLKI SEKMPVVAEKYFGGTD--DPAKRKOLF 415
QY 441 MIVQDQATVYATLOTAHYHRDAGLPVLYEYEHARGI-IVKPRTDGADHGVNVPFG 499
Db 416 QDLVADVIFGVSPVWVSRHRDAGAPTFMFEYRPSFVSAMRPKTVIGDHGDELFSVFG 475
QY 500 GPFATGLSGKKEKALSLQWVKYWANFARTGNPDGNLPCWPRYNKDEKYLQLDFTTRYGM 559
Db 476 SPLKDGASEEETNLKWKYKWFANFARNGSPNGGGLPHWPEYDQKEGYLKIGASTQAAQ 535
QY 560 KLUKEKQWAFMSLYQORPEK 580
Db 536 RLKDKVAFWSELRAKEAAEE 556

RESULT 3
ESTL_HUMAN STANDARD; PRT; 567 AA.
ID AC P23141; Q00015; Q13657; Q14062; Q16737; Q16788; Q9JULY2;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Liver carboxylesterase precursor (PC 3.1.1.1) (Acyl coenzyme
A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine
esterase) (HWE) (Serine esterase 1) (Brain carboxylesterase hBrl).
GN CES1 OR CES2 OR SES1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=92011649; PubMed=1918003;
RA Munger J.S., Shi G.P., Mark E.A., Chin D.T., Gerard C.,
Chapman H.A.;
RT "A serine esterase released by human alveolar macrophages is closely
related to liver microsomal carboxylesterases."
RL J. Biol. Chem. 266:18832-18838(1991).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=94032283; PubMed=8218228;
RA Kroetz D.L., McBride O.W., Gonzalez F.J.;
RT "Glycosylation-dependent activity of baculovirus-expressed human
liver carboxylesterases: cDNA cloning and characterization of two
highly similar enzyme forms."
RL Biochemistry 32:11606-11617(1993).
RN [3]
SEQUENCE FROM N.A.
RP TISSUE=Peripheral blood, and Placenta;
RC MEDLINE=94010913; PubMed=8406473;
RA Shibata F., Takagi Y., Kitajima M., Kuroda T., Omura T.;
RT "Molecular cloning and characterization of a human carboxylesterase
gene."
RL Genomics 17:76-82(1993).
RN [4]
SEQUENCE FROM N.A.
RP

RC TISSUE=Liver;
RX MEDLINE=94325258; PubMed=8049197;
RA Becker A., Bottcher A., Lackner K.J., Fehringer P., Notka F.,
Aslanidis C., Schmitz G.;
RT "Purification, cloning, and expression of a human enzyme with acyl
coenzyme A: cholesterol acyltransferase activity, which is identical
to liver carboxylesterase."
RL Arterioscler. Thromb. 14:1346-1355(1994).
RN [5]
SEQUENCE OF 1-429 FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=99448370; PubMed=10518925;
RA Mori M., Hosokawa M., Ogasawara Y., Tsukada E., Chiba K.;
RT "cDNA cloning, characterization and stable expression of novel human
brain carboxylesterase."
RL FEBS Lett. 458:17-22(1999).
RN [6]
SEQUENCE OF 61-567 FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=91148424; PubMed=197784;
RA Long R.W., Calabrese M.R., Martin B.M., Pohl L.R.;
RT "Cloning and sequencing of a human liver carboxylesterase isoenzyme."
RL Life Sci. 48:PL43-PL49(1991).
RN [7]
SEQUENCE OF 64-567 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91300111; PubMed=2070086;
RA Zschunke F., Salmassi A., Kreipe H., Buck F., Parwaresch M.R.,
Radzun H.J.;
RT "cDNA cloning and characterization of human monocyte/macrophage
serine esterase-1."
RL Blood 78:506-512(1991).
RN [8]
SEQUENCE OF 114-567 FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=92084150; PubMed=1749313;
RA Riddles P.W., Richards L.J., Bowles M.R., Pond S.M.;
RT "Cloning and analysis of a cDNA encoding a human liver
carboxylesterase."
RL Gene 108:289-292(1991).
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
activation of ester and amide prodrugs. Hydrolyzes aromatic and
aliphatic esters, but has no catalytic activity toward amides or a
fatty acyl CoA ester.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M73499; AAA35649.1; -
DR EMBL; L07764; AAA16036.1; -
DR EMBL; L07765; AAA35711.1; -
DR EMBL; D21088; BAA04650.1; -
DR EMBL; D21075; BAA04650.1; JOINED.
DR EMBL; D21076; BAA04650.1; JOINED.
DR EMBL; D21077; BAA04650.1; JOINED.
DR EMBL; D21079; BAA04650.1; JOINED.
DR EMBL; D21080; BAA04650.1; JOINED.
DR EMBL; D21081; BAA04650.1; JOINED.
DR EMBL; D21082; BAA04650.1; JOINED.
DR EMBL; D21083; BAA04650.1; JOINED.
DR EMBL; D21084; BAA04650.1; JOINED.
DR EMBL; D21085; BAA04650.1; JOINED.
DR EMBL; D21086; BAA04650.1; JOINED.
DR EMBL; D21087; BAA04650.1; JOINED.
DR EMBL; AB025026; BAA84995.1; -

DR EMBL; S73751; AAC60631.2; -
DR EMBL; M55509; AAA35650.1; -
DR EMBL; X52973; CAA37147.1; -
DR EMBL; M65261; AAA83932.1; -
DR PIR; A41010; A41010.
DR HSP; P21836; IMAH.
DR Genew; HGNC:1863; CES1.
DR MM; I14835; -
DR GO; GO:0004759; F:serine esterase activity; TAS.
DR GO; GO:0008152; P:metabolism; TAS.
DR GO; GO:0009636; P:response to toxin; TAS.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family; Polymorphism.
FT SIGNAL 1 18
FT CHAIN 19 567
FT ACT_SITE 221 221 LIVER CARBOXYLESTERASE.
FT ACT_SITE 221 221 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 468 468 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 564 567 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 18 18 G -> CA.
FT VARIANT 75 75 /FTID=VAR_002357.
FT VARIANT 75 75 S -> N (in dbSNP:2307240).
FT VARIANT 199 199 /FTID=VAR_014314.
FT VARIANT 203 203 R -> H (in dbSNP:2307243).
FT VARIANT 203 203 D -> E (in dbSNP:2307227).
FT VARIANT 362 362 /FTID=VAR_014595.
FT CONFLICT 4 7 Missing.
FT CONFLICT 12 12 /FTID=VAR_002358.
FT CONFLICT 17 17 RAPI -> PALV (IN REF. 3).
FT CONFLICT 17 17 W -> WA (IN REF. 2).
FT CONFLICT 56 56 A -> G (IN REF. 2).
FT CONFLICT 56 56 R -> G (IN REF. 7).
FT CONFLICT 115 115 D -> H (IN REF. 8).
FT CONFLICT 186 186 R -> G (IN REF. 7).
FT CONFLICT 281 281 R -> A (IN REF. 8).
FT CONFLICT 301 317 MKFLSLDQDPPRESQP -> IGNSYLTWYRETQREST (IN REF. 8).
FT CONFLICT 337 337 A -> R (IN REF. 8).
FT CONFLICT 383 390 WKSYPVLC -> GSPIPLFA (IN REF. 8).
FT CONFLICT 417 417 F -> I (IN REF. 8).
FT CONFLICT 512 512 E -> K (IN REF. 8).
FT CONFLICT 536 536 A -> G (IN REF. 2).
FT CONFLICT 563 563 E -> D (IN REF. 8).
SQ SEQUENCE 567 AA; 62521 MW; D3A00BDCDC7E5DFF CRC64;
Query Match 40.2%; Score 1251; DB 1; Length 567;
Best Local Similarity 44.2%; Pred. No. 6,9e-92;
Matches 250; Conservative 111; Mismatches 192; Indels 12; Gaps 9;
QY 26 WILCSLTLCLMAQTALGALHTKRPQW-TKGTGLQK--QMHVGKTIQVFLGVFFSRP 82
DB 2 WLRAFLA-TLSASAAG--HSSPPVDTVHGKLVKFLVSLGPAQPAIFLGIPIPAKP 58
QY 83 PLGILFAPPEPPEPKGTRDATTTPGCLQF-SWGQLASMTVSTRERYKWLRFSDCLY 141
DB 59 PLGPLRFTPPQAPBPSFVNKATSTVPPMCTQPKAGQLLSLFTNRKNINPLKSEDCLY 118
QY 142 LNVYAPARAFPGDPQLPVMVWFFGGAFIVGAASYSGLAAREKVVLFLOHRLGIPGFL 201
DB 119 LNIYTPADLTKNRLEFVMVWIHGGGLMVGAASTYDGLALAHENVVVVIQYRLGIWGF 178
QY 202 STDDSHARGNGLLDQMAALRVQENIAAFAGDPDGNVTLFGSAGAMSISGLMSPPLASG 261
DB 179 STGDSHRGNWGHLDQVAALRVQDNIAFGNPGSVTFIGSGAGGSVSLVLSPLAKN 238

262 LFHRAISQSGTALPRLFITSNPLK-VARKVAHLAGCNHNSTQILVNCRLASLGTKMRVS 320
239 LFHRAISQSGVALTSVLVKGKGVKPLAEIAITAGCKTTTSAVMVHCLRQKTEBELLETT 298
321 NKMFELQINFORDEPBEIINWSMPVVDGVPIDPDLVLLTGKGVSSYPYLLGVNLSFNL 380
299 LKMKFLSLDQDPPRESQPLIGTVIDGMLLKLTPPELQAEENFHTVPMVGVINKQSPGWL 358
381 LP-YIMKFPPLNRQAMKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNNEHDKMLNR 439
359 IPVQLMSYPLSEGQDQKTAMSLWKSYPVLCIAKELIPEATEKYLGGTD--DTVKKDL 416
440 MMDIVQDATFVYATLQTAHYHRRDAGLVPVLYFEHH-ARGIIVKPRTDGADHGDMEYFLF 498
417 FLDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSDMKPKTVIGDHGDELFSVF 476
499 GGPATGLSGKKEKALSLOWMYWANFARTGNPDGNLPCWPNYKDEKYLQDLDTFRVG 558
477 GAPFLKGAEEBETRLSKVMYKFWANFARNNGENGLPHWPEYNQKGYLQICANTQAA 536
559 MKLKEKMAFMSLYQSRPEKORQ 583
537 QKLXDKVEAFWNLFAKKAKEKPPQ 561

RESULT 4
ESTL_PIG STANDARD; PRT; 566 AA.
AC Q29550;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Liver carboxylesterase precursor (EC 3.1.1.1) (Proline-beta-naphthylamidase).
DE naphthylamidase).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92070571; PubMed=1959668;
RA Matsushima M., Inoue H., Ichinose M., Tsukada S., Miki K., Kurokawa K., Takahashi T., Takahashi K.;
RA "The nucleotide and deduced amino acid sequences of porcine liver proline-beta-naphthylamidase. Evidence for the identity with carboxylesterase.";
RT FEBS Lett. 293:37-41(1991).
RL
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the activation of ester and amide prodrugs.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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EMBL; X63323; CAA44929.1; -
PIR; S19307; S19307.
DR HSP; P21836; IMAH.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW

KW Signal; Multigene family.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT CHAIN 19 566 LIVER CARBOXYLESTERASE.
 FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 467 467 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 88 117 BY SIMILARITY.
 FT SITE 274 285 BY SIMILARITY.
 FT CARBOHYD 563 566 PREVENT SECRETION FROM ER (POTENTIAL).
 FT SITE 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 566 AA; BE046545307DEDES CRC64;

Query Match 39.8%; Score 1239.5; DB 1; Length 566;
 Best Local Similarity 44.2%; Pred. No. 5.6e-91;
 Matches 248; Conservative 110; Mismatches 192; Indels 11; Gaps 7;

QY 26 WILCWSLTLCLMAQTALGALHTKRPQW-TKYGTLOGKQWVG--TKPIQVFLGVFPFSP 82
 DB 2 WLL--PLVLTSLASSATWAGQAPSPVDTAQRVLGVKYSLEGLAQPVAVLGVFPFAP 59

QY 83 PLGILPAPPEPPEPWKIRDTATYPGCIQESGQ--LASMYVSTRERYKMLRSEDCL 140
 DB 60 PLGSLRFAFPQAPAEPSFVKNTTSYPPMCQDPVEQMTSDLFTNGKERLT-LEFSEDCL 118

QY 141 YLNVYAPAPAGDPQLPVMVWPPGGAFIVGAASSYEGSDLAAREKVVLVFLQHLGIFG 200
 DB 119 YLNIYTPADLTKEGRPLVMVWIHGGGLVLCGAPMVGVLAAHENVVVAIQVRLGIFG 178

QY 201 LSTDDSHARGNWGLLQMAALRWQENIAAFGDPGNVTLFGQAGAMSISGLMSPLAS 260
 DB 179 FSTGDEHSRGNWGHLDQVAALHWQENIANFNGDPSGVITFGESAGGESVSVLVLSPLAK 238

QY 261 GLFHRAISQSGTALFRLFTSNPLKVAKVLAHAGCNHNSQLVNCRLASLSTKVMRVS 320
 DB 239 NLFHRAISEGVALTVALKVKQWAAKQAVLAGCKTTTSAVFHCLQKSEDELLDT 298

QY 321 NKRFQLNQRDPEEIIWMSVVDGWIPIPDPLVLLTQGVSSVPYLLGVNNLEFNNWL 380
 DB 299 LKMKFELTDPHGDORESHPLPTVVDGVLKPKMPEILAEKQNTVPIVINGKQEFGL 358

QY 381 LPVIMKPLNQAMRKETITKMLWSTRTLLNITKEQVPLVVEYLDNVNHEHDKMLNRNM 440
 DB 359 LPTMGPFLSEGLDKDQKATSLKWSYPIANIPEELTPVATDKYLGTDTPVKK--KDLF 416

QY 441 MDVQVQATFYVATQAHYHRDAGLPVLYLVEFHH--ARGIIVKPRTDGADHGDVYFLFG 499
 DB 417 LDLMGVVFPVSVTVARQHRDAGATYMYEFOYRFSFSDKPKTVIGHGDEIFSVFG 476

QY 500 GPATGLSMGKALKSLQMMKYWANFARTGNPDGNLPCWPYRNKDEKYLQDLDTTRVGM 559
 DB 477 FPLLKGDAPPEEVSLSKTVMKFWANFARSGNPNGEGLPHWPMYDQEGYLQIGVNTQAAK 536

QY 560 KLKEKMAFWMSLYQSORPEK 580
 DB 537 RLKGEVAFWNDLLSKEAAKK 557

RESULT 5
 EST3 RAT ID EST3 RAT ID EST3 RAT ID EST3 RAT ID EST3 RAT ID EST3 RAT ID
 AC Q63106; STANDARD; PRT; 561 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxylesterase ES-3)
 DE (pI 5.5 esterase) (ES-HTEL).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RX SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95032008; PubMed=7945287;

RA Robbi M., Beaufay H.;
 RT "Cloning and sequencing of rat liver carboxylesterase ES-3 (egasyn).";
 RL Biochem. Biophys. Res. Commun. 203:1404-1411(1994).
 CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
 CC activation of ester and amide prodrugs.
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
 CC reticulum.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC
 CC EMBL; X81395; CAA57158.1; -.
 DR PIR; JC2447; JC2447.
 DR HSSP; P21836; IMAA.
 DR InterPro; IPR002018; CarbesteraseB.
 DR InterPro; IPR003379; Ser esters.
 DR Pfam; PF00135; Coesterase_1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 DR Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
 KW Signal; Multigene family.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT CHAIN 19 561 LIVER CARBOXYLESTERASE 3.
 FT ACT_SITE 221 221 BY SIMILARITY.
 FT ACT_SITE 466 466 BY SIMILARITY.
 FT DISULFID 87 116 BY SIMILARITY.
 FT DISULFID 273 284 BY SIMILARITY.
 FT SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 489 489 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 561 AA; 61714 MW; 1E14D66DF098986F CRC64;

Query Match 38.7%; Score 1205.5; DB 1; Length 561;
 Best Local Similarity 43.3%; Pred. No. 2.9e-88;
 Matches 238; Conservative 114; Mismatches 191; Indels 7; Gaps 6;

QY 28 LC-WSLTCLNAQTALGALHTKRPQWTKYGTLOGKQWVG-GKT-PIQVFLGVFPFSPPL 84
 DB 1 MCLRALILVFLAAATAGGHPSLPVDTLQGVKLVGSDEGTPQVAVFLGVFPFAPPL 60

QY 85 GILRFAFPPEPPEPWKIRDTATYPGCIQES-WGQLASMYVSTRERYKMLRFSDECLYN 143
 DB 61 GSLRFAFPQAPAEPSFVKNTTSYPPMCQDPVAGQIVNDLLTNWEENISLQFSEDCLYN 120

QY 144 VYAPARAGDPQLPVMVWPPGGAFIVGAASSYEGSDLAAREKVVLVFLQHLGIFGLST 203
 DB 121 IYTPADLTKEGRPLVMVWIHGGGLVLCGASTYDGLALSTHENVVVVIQVRLGIFGLST 180

QY 204 DSHARGNWGLLQMAALRWQENIAAFGDPGNVTLFGQAGAMSISGLMMSPLASGLF 263
 DB 181 GDEHSRGNWGHLDQVAALHWQENIDNFGDPSGVITFGESAGGESVSVLVLSPLAKNLF 240

QY 264 HRAISQSGTALFRLFTSNPLKVAKVLAHAGCNHNSQLVNCRLASLSTKVMRVSNM 323
 DB 241 HKAISESGVALTAGLVKKNTRPLAEKIAVWSGCKSTTSASMVHCLQKTEBELLETLKL 300

QY 324 RFLQNFQDPEEIIWMSVVDGWIPIPDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY 383
 DB 301 NLFSLDLHGDGRQSPVFPVTVLDGVLPKXPEEILAEKDFNTVPIYVINGKQEFGLPT 360

QY 384 IMKFFLANRQAMRKETITKMLWSTRTLLNITKEQVPLVVEYLDNVNHEHDKMLNRNMDI 443
 DB 361 MNVPPSDMKLDPMTATSLKKSSFLNLPPEAIPVAEIKYLRHTDDPDRN--KDQLLEL 418

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QY 444 VQATFVATLQTAHVHRDAGLPVLYEPEHH-ARGIIIVKPRDGDADHGDGEMVFLFGPPF 502
D 419 IGVIFGVPSVIVSRGHRDAGATYMYEQYRPSFSKMKPSTVVGHDGDEIYSYFGAPI 478
QY 503 ATGLSMGKALSLQWKYWANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGMK 562
D 479 LRGTGSKKEEINLSMMKFWANFARNNGQGLPHWPEYDQKEGYLQIGATTQQAQK 538
QY 563 EKKMAFWMSL 572
D 539 EKEVAFWSEL 548

RESULT 6
ID ES22 MOUSE STANDARD; PRT; 562 AA.
AC Q64176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 22 precursor (EC 3.1.1.1) (Egase) (Esterase-22) (Bs-22).
DE GN ES22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92147141; PubMed=1783403;
RA Heintz N., Swank R.T., Fletcher C., Zhen L., Novak E.K., Baumann H.,
RA Owitz N., Ganschow R.E.;
RT "Characterization and functional expression of a cDNA encoding egasyn
RT (esterase-22): the endoplasmic reticulum-targeting protein of beta-
RT glucuronidase."
RL Genomics 11:956-967(1991).
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
CC activation of ester and amide prodrugs.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC ENBL; S80191; AAB21335.1; -.
CC PIR; A55281; A55281.
CC HSP; P21836; 1W4H.
CC MGD; MGI:95432; ES22.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000379; Ser_estr.
CC Pfam; PF00135; Coesterase; 1.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 19 BY SIMILARITY.
FT CHAIN 20 562 LIVER CARBOXYLESTERASE 22.
FT ACT_SITE 222 222 BY SIMILARITY.
FT ACT_SITE 467 467 BY SIMILARITY.
FT DISULFID 88 117 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC. .) (POTENTIAL).

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SQ SEQUENCE 562 AA; 61581 MW; F81A4367A0CCB2E3 CRC64;
Query Match 38.7%; Score 1205.5; DB 1; Length 562;
Best Local Similarity 42.4%; Pred. No. 2.9e-88;
Matches 241; Conservative 119; Mismatches 188; Indels 21; Gaps 9;
QY 28 LCWS-LTLCMAQTALGALHTKEPQVVTYKGTLOGQMHVGK-----TPIOVLGVP 78
D 1 MCLGALILVSLAFTAGAGHPSPDWV---DTVQGVK--GKIYISLEGFTQPVAVFLGVP 55
QY 79 FSREPLGILRFAPPEPEPEPKGIRDATTYPGCLQES-WGQLASMYVSTRERYKWLRFSE 137
D 56 FAXPPLGLSLRFAPPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE 115
QY 138 DCLYLVNYAPAPAPDQPLPMWVWFFGGAFIVGAASYESGDLAAREKVLVFLQHLGI 197
D 116 DCLYLVNIYTPADLTSTKDRPLPMWVWVHGGGLVGLGASTYDGLVLTSTHENVVVVVIQRLGI 175
QY 198 FGFLSTDDSHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMSP 257
D 176 WGFSTGDEHSRGNWGHLDQVAALHWQDNIAKFGGDPGSGVTIFGESAGGESVSVLVLP 235
QY 258 LASGLFRAISQSGTALFRUITSNPLKVAKVAHLAGCHNHNSTOILVNCRLALSTKVM 317
D 236 LAKNLFQRAISEGVALTAGLVKNTPLAEKIAVISGCKNTTSAAMVHCLRQKTEELL 295
QY 318 RVSNKMFLOLNFOROPEEIIWSMSPVWDGWIPTDPLVLLTQGVSSVPYLLGVNLEF 377
D 296 GTTLKLNLFKLDLHGDSTRQSHPFVPTVLDGLVLPKMPPEELAEKNFTVPIYVIGINKQEF 355
QY 378 NWLPLPYINKPLNRQAMKRTITMLMSTETLNTKEQVPLVVEYLYDNVNEHDK-ML 436
D 356 GWILPTWNTYPPSDVKLDQMTAMSLKSSFLNLPEDALVAIEKYL---RDKYTGREN 412
QY 437 RNRWMDIVQDATFYATLQTAHVHRDAGLPVLYEPEHH-ARGIIIVKPRDGDADHGD 495
D 413 KDQLELIGDGVVGVPSVIVSRGHRDAGATYMYEQYRPSFSSEMKPDTVVGHDGDEIY 472
QY 496 FLFGGPPATGLSMGKALSLQWKYWANFARTGNPDGNLPCWPRYNKDEKYLQDFTT 555
D 473 SVFGAPILRGTSSEEEINLSMMKFWANFARNNGQGLPHWPEYDQKEGYLQIGATT 532
QY 556 RVGKLEKEKMAFWMSLY-OSQPEKORQ 583
D 533 QQAQKLEKEVAFWTELLAKKQLPTEHT 561

RESULT 7
EST5_RAT
ID EST5_RAT STANDARD; PRT; 561 AA.
AC Q63010;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase B-1 precursor (EC 3.1.1.1) (Liver microsomal
DE carboxylesterase). (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sorague-Dawley; TISSUE=Liver;
RX MEDLINE=95050819; PubMed=7961958;
RA Yan B., Yang D., Brady M., Parkinson A.;
RT "Rat kidney carboxylesterase. Cloning, sequencing, cellular
RT localization, and relationship to rat liver hydrolase."
RL J. Biol. Chem. 269:29688-29696(1994).
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
CC activation of ester and amide prodrugs.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic

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CC reticulum.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U10698; AAA64639.1; -.
DR HSP; P21836; IMAA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000886; ER_target_5.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 561
FT ACT_SITE 221 221
FT ACT_SITE 466 466
FT DISULFID 87 116
FT DISULFID 273 284
FT SITE 558 561
FT CARBOHYD 79 79
SQ SEQUENCE 561 AA; 62494 MW; 013C1C3ACEB6C9 CRC64;

Query Match 38.2%; Score 1187.5; DB 1; Length 561;
Best Local Similarity 41.1%; Pred No 7.8e-87;
Matches 230; Conservative 123; Mismatches 196; Indels 11; Gaps 5;

QY 24 MRWILCWSLFLCMA--QPALGALHTKRPQVWTKYGLQCKQMHGKTPIQVFLGVPSR 81
DB 3 LRSLFLVSLATVCVGNPSPVVDVTKGKGLKVASLEGVTSVA-----VELGVPPAK 57
QY 82 PPLGILRFAPPEPEPKGIRDATTYPGCLQESW-GQLASVMVSTREYKMLRSEDC 140
DB 58 PPGSLRFAPPAEPEWPFVNTTTPPCSDATKGQNRNDLLTNKKEKVLHQSEDC 117
QY 141 YLVNYPAPAPGDPQLPVMVWFFGGAFIVGAASVEGSDLAAREKVVFLQHRIGIFG 200
DB 118 YLVNIYPADFTKDRNPVMVWIHGGGLTGGASTYDQVLSAYENVVVAIQVRLGIWGF 177
QY 201 LSTDDSHARGNGLLDQMAALRWQENIAAFGDPGNVTLFGOSAGAMISGLMMSPLAS 260
DB 178 FSTGDEHSRGNWGHLDQVAALHWQDNIAFNGDPSGVTIFGESAGGFSVSLVLSPLSK 237
QY 261 GLFHRAISQGTALFRFLITSNPLKVAKVVAHLACGNHNSITLVNCLRALSGTKMVRVS 320
DB 238 NLVHRAISEGVVLTFLTKDVRPAKQIADWAGCKTTSALIVHCLRQKTEELLEIM 297
QY 321 NKVRFLQNFQRPDEIILMSNPVDPGWIPDPLVLLTQGVSSVPYLLGVNNLEFNWL 380
DB 298 EKVNLIKLSQSDTKESYHFLSTVIDVWLPKDPKEILAEKQNPVTPYIVGINKQECGWL 357
QY 381 LPVIMKPLNQRAMKETITKMLWSITLJLNITKEQVPLVVEYLDNVNEHMKMLNRM 440
DB 358 LPTNMRFPVDPVLDKXKQAMLEKFAISYIGIEDIIPVAIEKY--RKSGDDPIKIRGI 415
QY 441 MDIVQDPTFYATLQTAHYHRDAGLPVLYYEFPHH-ARGIIVKPRDTGDHGDHMYFLFG 499
DB 416 LAFIGDVLFCIPSVNMSRDRDAGAPTYVYVYQYFSPSPQRPKDVGDHADDVYVFG 475
QY 500 GPATGLSMCKEKAISLQMKYKWFANFARTGNPDGNLPCWPRYNKDEKYLQIDFTIRGM 559
DB 476 APILRDGAEEETKLSQWVKFWANFARNGNPNARGLPHPQPDYQKBEYLQIGATTQQSQ 535
QY 560 KLKEXKMAFWNSLYQSQRPE 579
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Db 536 RLKAEVAFWTLAKRQPQ 555
RESULT 8
ID EST4 RAT STANDARD; PRT; 561 AA.
AC Q64573; Q62679;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 4 precursor (EC 3.1.1.1) (Carboxylesterase ES-4)
DE (Microsomal palmitoyl-CoA hydrolase) (Kidney microsomal
DE carboxylesterase) (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96190723; PubMed=8611161;
RA Robbi M., van Schaftingen E., Beaufay H.;
RT "Cloning and sequencing of rat liver carboxylesterase ES-4
RT (microsomal palmitoyl-CoA hydrolase).";
RL Biochem. J. 313:821-826(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95050819; PubMed=7961958;
RA Van B., Yang D., Brady M., Parkinson A.;
RT "Rat kidney carboxylesterase. Cloning, sequencing, cellular
RT localization, and relationship to rat liver hydrolase.";
RL J. Biol. Chem. 269:29688-29696(1994).
CC -!- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
CC ACTIVATION OF ESTER AND AMIDE PRODRUGS. HYDROLYSES OMICRON-
CC NITROPHENYL ACETATE AND ALPHA-NAPHTHYL ACETATE. IT ALSO
CC HYDROLYSES ACETANILIDE AND, DISTINCTIVELY, PALMITOYL-COA.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X81825; CAA57419.1; -.
DR EMBL; U10697; AAA64638.1; -.
DR PIR; S62788; S62788.
DR HSP; P21836; IMAA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000886; ER_target_5.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 561
FT ACT_SITE 221 221
FT ACT_SITE 466 466
FT DISULFID 87 116
FT DISULFID 273 284
FT SITE 558 561
FT CARBOHYD 79 79
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FT CONFLICT 7 7 I -> F (IN REF. 2).
FT CONFLICT 60 60 L -> P (IN REF. 2).
FT CONFLICT 213 213 G -> A (IN REF. 2).
FT CONFLICT 253 253 P -> T (IN REF. 2).
FT CONFLICT 310 311 DN -> IT (IN REF. 2).
FT CONFLICT 342 342 T -> N (IN REF. 2).
FT CONFLICT 425 426 SI -> FY (IN REF. 2).
FT CONFLICT 509 509 G -> A (IN REF. 2).
FT CONFLICT 553 553 Q -> E (IN REF. 2).
SQ SEQUENCE 561 AA; 62274 MW; EDF48F3309521C79 CRC64;

Query Match 38.1%; Score 1184.5; DB 1; Length 561;
Best Local Similarity 41.7%; Pred. No. 1.3e-86;
Matches 234; Conservative 123; Mismatches 191; Indels 13; Gaps 7;

QY 24 MRWILCWSLTCLM--AQTALGALHTKRPQVVTKYGTLOGKQWHVGKTPIQVFLGVPPSR 81
DB 3 LSELLVSLATCVVYGNPSSPPVVDITKGVLGKYYVLEGVTSVA-----VFLGVPPAK 57

QY 82 PPLGILRFAPPEPPKQIRDTATTPPGCLQE-SWGLASMYVSTREYKWLRSDECL 140
DB 58 PPLGSLRFAPQAPSPVFNKTTTPPMCSQDAKQGRMDLLTNKKEIHLFESECL 117

QY 141 YLVNYPAPAPGPPQPLPMVWPFPGAFIVGAASSYEGSDLAAREKVVFLQHRIGIFG 200
DB 118 YLVNYPADFTKNSRLPVMVWIHGGMTLGGASTYDGRVLSAYENVVVVAIQVRLGNGF 177

QY 201 LSTDDSHARNGWGLDQMAALRWQENIAAFGGDPGNVTLFGSAGAMISGLMSPAS 260
DB 178 FSTGDEHSRNGWGLDQVAALHWQDNIAFNGDPGVTIFGESAGGSVVLVLSPLTK 237

QY 261 GLFHRAISQGTALFRLFTSNPLKVAKVLAHLAGCNHNSTOILVNCLEALSGTKVMVS 320
DB 238 NLFHRAISESGVFLPOLLTKVVRPAKQIADWAGCETTSLIIVHCLKQKTEBSELLEIM 297

QY 321 NKKEFLQNLNRPDPEEIIISMSPVVDGVIPDDPLVLTQGVKSVYPYLLGVNNLEFNWL 380
DB 298 KKNVLIKSSQDNKESYHLSFSTVDNVVLFPDKEILAEKNFTVPYIVGINKQCGWL 357

QY 381 LPVIMKF-PLNRQAMKEITITMLSTRLLNITKQVPLVVEEYLDNVNEDWKLNR 439
DB 358 LPTMGVFPADVLDKMAIT-LLEKFASLYGIPEDIIPVAIEKY--RKGSDSTKIRDG 414

QY 440 MMDIVQATVYATLTQAHVHRDAGLPVLYEPEHH-ARGITVPRPTGDAGHGDWYFLF 498
DB 415 ILAFIGDVSFISVMVRDHRDAGATPYEYQYVFPSSQRPKHVVGDDHADDLYSVF 474

QY 499 GGPFTGLSMGKEKALSQMKWYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVG 558
DB 475 GAPILRDGASEEIKLSKVMKFWANFARNGNRGLPFWFDQDQKEEYLQIGATTQOS 534

QY 559 MKLKKKQVAPWMSLYQSORE 579
DB 535 QRLKASEVAPWTQLAKRPQ 555

RESULT 9
EST1_RAT STANDARD; PRT; 549 AA.
AC P1059; Q63106; Q64626;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 1 precursor (EC 3.1.1.1) (Carboxylesterase ES-1) (E1) (ES-THET).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 19-48.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=89174514; PubMed=3235453;
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RA Takagi Y., Morohashi K., Kawabata S., Go M., Omura T.;
RT "Molecular cloning and nucleotide sequence of cDNA of microsomal
RL carboxylesterase E1 of rat liver.";
RN J. Biochem. 104:801-806(1988).
RP [2]
RX SEQUENCE OF 10-549 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=9050119; PubMed=2973315;
RA Long R.M., Satoh H., Martin B.M., Kimura S., Gonzalez F.J., Pohl L.R.;
RT "Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence
RL for a multigene family.";
RN Biochem. Biophys. Res. Commun. 156:866-873(1988).
RP [3]
RX SEQUENCE OF 13-549 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=94274701; PubMed=8006016;
RA Alexson S.E.H., Finlay T.H., Hellman U., Svensson L.T., Diczfalussy R.,
RT Eggertsen G.;
RT "Molecular cloning and identification of a rat serum carboxylesterase
RL expressed in the liver.";
RN J. Biol. Chem. 269:17118-17124(1994).
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
CC activation of ester and amide prodrugs.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC EMBL; M20629; AAA40871.1; -
DR EMBL; D30620; BAA06310.1; -
DR EMBL; D00362; BAA20565.1; -
DR EMBL; X78489; CAA55241.1; -
DR FIR; A31584; A31584.
DR HSPF; P21836; IMAH.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 549 LIVER CARBOXYLESTERASE 1.
FT ACT_SITE 221 221 BY SIMILARITY.
FT ACT_SITE 453 453 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 546 549 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 372 372 P -> L.
FT CONFLICT 48 48 A -> R (IN REF. 3).
FT CONFLICT 174 175 IW -> FG (IN REF. 2).
FT CONFLICT 250 250 V -> L (IN REF. 1).
FT CONFLICT 399 399 K -> N (IN REF. 1).
FT CONFLICT 504 504 K -> E (IN REF. 1).
FT CONFLICT 512 513 LQ -> FE (IN REF. 3).
SQ SEQUENCE 549 AA; 60174 MW; 18D6A586DA50E662 CRC64;

Query Match 37.3%; Score 1161.5; DB 1; Length 549;
Best Local Similarity 42.6%; Pred. No. 8.9e-85;
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Matches 240; Conservative 105; Mismatches 191; Indels 27; Gaps 9;

QY 26 WI--LCW-SLTLCM--AQTALGALHTKRPQVTKYGTLOGKQMHVGTPIQVFLGVPPFS 80
 Db 2 WLCALWASLAVCPVWHPSPVVDITKGVKGVSLGFTQ-----PVAVFLGVPPFA 56

QY 81 RPPGILRFAPEPPEPPKMGIRDTATYPGCLQBS-WGQLASMYVSTREYKWLRFSEDC 139
 Db 57 KPFLGSLRFAPEPPEPWSFVNTTTPPMCSQDGVVVKLLADMLSTGKESIPLEFSEDC 116

QY 140 LYLNVYAPARAPGPDPQVPMVWFGGAFIVGAASYEGSLAAREKVVLVFLQHRIGFG 199
 Db 117 LYLNIYSPADLTGKSLPVMVWVHGGGLIIGGASPSGLALSARENVVVVIQYRLGIWG 176

QY 200 FLSTDDSHARGNWGLDQMAALRWQENIAAFGDPGNVTLFGOSAGAMSISGLMMSPLA 259
 Db 177 LFTSGDEHSRGNWAHLQDLAALRWQENIAFGNPDVSVTFGSSGGISVSVLVLPLG 236

QY 260 SGLFHRAISQSGTALFRFLTITSNPLKVAKVHAHLAGNHNSTQILVNCRLALSQTVMRV 319
 Db 237 KNLFHRAISESGVVLITNLDKNTQVAQMIALSGCNETSSAAMVQCLRAQ-----287

QY 320 SNKMRFLQNFQRPDEEIIWMSPVVDGVIPDDPLVLLTGQKVSVPYLLGVNNLEFNW 379
 Db 288 KTEAELELTVKLDNT-----SMSTVDGVVLPKTPPEILTEKSFNTVPIVGNKQBFGW 343

QY 380 LLPYIMKFPNLRQAMRKETITKMLWSTRLNITKEQVPLVWBEYLDNVNEHDKMLRNR 439
 Db 344 IIPMGNLLSEGMNEKMASSFLKRPSPNLNISESVIPAIEKILRGTDPAKK--XEL 401

QY 440 MMDIVQDQATFYATLQTAHYHRDAGLPVLYVEFEHARGII-VKPRTDGADHDEMFLF 498
 Db 402 LLDWFSVDFGIPAVLWRSRLRDAQATYMEFYQRPFSVSDQRPQTVGDHDEIFSVF 461

QY 499 GGPFATGLSMGKALKSLQMKYWANPARTGNPDNGLPCWRYNKDEKYLQDFTTRVG 558
 Db 462 GTPELKEGASEETNLSKLVKFWANFARNNGENGEGLPWPYDQEGYLGQIGATTQQA 521

QY 559 MKLKEKQKAWMSLYQSQREPKQ 581
 Db 522 QKLKEEVAFWFTELLAKNPQTE 544

RESULT 10
 ESTN MOUSE
 ID ESTN MOUSE STANDARD; PRT; 554 AA.
 AC P23953;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Liver carboxylesterase precursor (EC 3.1.1.1) (PES-N).
 GN ESI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=91169540; PubMed=1840565;
 RA Ovinic M., Tepperman K., Medda S., Elliott R.W., Stephenson D.A.,
 RT "Characterization of a murine cDNA encoding a member of the
 RT carboxylesterase multigene family."
 RL Genomics 9:344-354(1991).
 CC -I- FUNCTION: Involved in the detoxification of xenobiotics and in the
 CC activation of ester and amide prodrugs.
 CC -I- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -I- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
 CC reticulum.
 CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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 CC -----
 CC EMBL: M57960; AAA63297.1; -
 CC PIR: A39060; A39060.
 CC HSP: P37967; IQE3.
 CC MGD: MGI:95420; Esl.
 CC InterPro: IPR002018; Carboxylesterase.
 CC InterPro: IPR000379; Ser esters.
 CC Pfam: PF00135; Coesterase; 1.
 CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 CC Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
 CC Signal; Multigene family.
 CC SIGNAL 1 18
 CC FT CHAIN 19 554
 CC FT ACT_SITE 21 221
 CC FT ACT_SITE 455 455
 CC FT DISULFID 87 116
 CC FT DISULFID 273 284
 CC FT SITE 551 554
 CC FT CARBOHYD 79 79
 CC FT CARBOHYD 274 274
 CC FT CARBOHYD 304 304
 CC FT CARBOHYD 377 377
 CC FT CARBOHYD 478 478
 CC FT SEQUENCE 554 AA; 61140 MW; 8A9260553DCCBF69 CRC64;
 SQ
 Query Match 36.7%; Score 1141.5; DB 1; Length 554;
 Best Local Similarity 41.5%; Pred. No. 3.5e-83;
 Matches 233; Conservative 113; Mismatches 190; Indels 25; Gaps 10;

QY 26 WI--LCW-SLTLCM--AQTALGALHTKRPQVTKYGTLOGKQMHVGTPIQVFLGVPPFS 80
 Db 2 WLCALWASLAVCPVWHPSPVVDITKGVKGVSLGFTQ-----PVAVFLGVPPFA 56

QY 81 RPPGILRFAPEPPEPPKMGIRDTATYPGCLQBS-WGQLASMYVSTREYKWLRFSEDC 139
 Db 57 KPFLGSLRFAPEPPEPWSFVNTTTPPMCSQDGVVVKLLADMLSTGKESIPLEFSEDC 116

QY 140 LYLNVYAPARAPGPDPQVPMVWFGGAFIVGAASYEGSLAAREKVVLVFLQHRIGFG 199
 Db 117 LYLNIYSPADLTGKSLPVMVWVHGGGLIIGGASPSGLALSARENVVVVIQYRLGIWG 176

QY 200 FLSTDDSHARGNWGLDQMAALRWQENIAAFGDPGNVTLFGOSAGAMSISGLMMSPLA 259
 Db 177 LFTSGDEHSRGNWAHLQDLAALRWQENIAFGNPDVSVTFGSSGGISVSVLVLPLG 236

QY 260 SGLFHRAISQSGTALFRFLTITSNPLKVAKVHAHLAGNHNSTQILVNCRLALSQTVMRV 319
 Db 237 KNLFHRAISESGVVLITNLDKNTQVAQMIALSGCNETSSAAMVQCLRAQ-----296

QY 320 SNKMRFLQNFQRPDEEIIWMSPVVDGVIPDDPLVLLTGQKVSVPYLLGVNNLEFNW 379
 Db 297 SKL--VOYNT-----SLSTMIDGVLPKAPAEILAEKSFNTVPIVGNKQBFGW 345

QY 380 LLPYIMKFPNLRQAMRKETITKMLWSTRLNITKEQVPLVWBEYLDNVNEHDKMLRNR 439
 Db 346 IIPMGNLLSEGMNEKMASSFLKRPSPNLNISESVIPAIEKILRGTDPAKK--SEL 403

QY 440 MMDIVQDQATFYATLQTAHYHRDAGLPVLYVEFEHARGII-VKPRTDGADHDEMFLF 498
 Db 404 ILDMFGDIFFGIPAVLLSRSLRDAGVSTYMEFYRPSFVSDKRPQTVGEGHGEIFFV 463

QY 499 GGPFATGLSMGKALKSLQMKYWANPARTGNPDNGLPCWRYNKDEKYLQDFTTRVG 558
 Db 464 GAPLLKEGASEETNLSKLVKFWANFARNNGENGEGLPWPYDQEGYLGQIGATTQQA 523

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QY 559 MKLKEKMAFWMSLYQSORPE 579
DB 524 QRLKAEVAFWTELLAKNPPE 544

RESULT 11
EST1_RABIT STANDARD; PRT; 539 AA.
AC P1237;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Liver carboxylesterase 1 (EC 3.1.1.1).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 1;
SEQUENCE, AND ACTIVE SITES SR=195 AND HIS-441.
RX MEDLINE=88139431; PubMed=3443253;
RA Korza G., Ozols J.
RT "Complete covalent structure of 60-kDa esterase isolated from
RT 2,3,7,8-tetrachlorodibenzo-p-dioxin-induced rabbit liver
RT microsomes."
RL J. Biol. Chem. 263:3486-3495 (1988).
RN 2;
SEQUENCE OF 1-70 AND 532-539.
RX MEDLINE=88033124; PubMed=3667634;
RA Ozols J.;
RT "Isolation and characterization of a 60-kilodalton glycoprotein
RT esterase from liver microsomal membranes."
RL J. Biol. Chem. 262:15316-15321 (1987).
CC -1- FUNCTION: Involved in the detoxification of xenobiotics and in the
CC activation of ester and amide prodrugs.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR PIR; A29923; A29923.
DR HSSP; P21836; 1MAH
DR InterPro; IPR002018; CarboxylesteraseB.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum.
FT ACT_SITE 195 195
FT ACT_SITE 441 441
FT DISULFID 69 98
FT DISULFID 247 258
FT SITE 536 539
FT CARBOHYD 61 61
FT CARBOHYD 363 363
FT CARBOHYD 539 AA; 59539 MW; 9BC72BC36A49B0BD CRC64;
SQ SEQUENCE 539 AA; 59539 MW; 9BC72BC36A49B0BD CRC64;

Query Match 36.4%; Score 1133; DB 1; Length 539;
Best Local Similarity 41.3%; Pred. No. 1.6e-82;
Matches 227; Conservative 115; Mismatches 177; Indels 30; Gaps 10;

QY 46 HTKEPQVVKYGTGQKMHVK-----TPIQVFLGVPPFRPPLGLIRFAPPPPP 97
DB 1 HPSAPPVV---DTVKGKVL--GKFSVLEGAQPVAVFLGVPPFAKPPGLSLRFAPPPAES 55

QY 98 WKGIRDATTYPGCLQE--SWGQASMYVSTRERYKWLRFSEDCLYINVTAPARAGDPQ 155
DB 56 WSHVKNTSYPPMCCSDAVSGHMLSELFTRNKENIP--LKFSEDCLYINVTADTLKRG 114

QY 156 LPVMWVPPGAFIVGASVYSGSLAAREKVLVFLQHLRIGIFGLSTDDSHARGNWGLL 215
DB 115 LPVMWVHGGGLMVGGASTYDGLALSARENVVVVIQYRLIGIGGFGENIDE-----L 166

216 DQMAALRWQENTAAFGGDPGNVTLFQSQAGAMSISGLMMSPLASGLFHRASISQSTALF 275
167 FLVAVNRWQDNIANFGGDPGVTIFGESAGGQSVSILLSPLTKNLFRHRAISESGVALL 226
276 RLFTTSNPLKVAKKVAHLACNHNSTQILVNCILRALSGTKVWVSNKMRFLQLNFORDPE 335
227 SSLFRKNTKSLAEKIAIEAGCKTTTSAVMVHCLQRQTEBELMEVTLKMKFMAJDLVGDDPK 286
336 EIIWMSPPVVDGVIPDPPLVLLTQGVSSVPYLLGVNNLEFNWLLP-YIMKFPPLNRQAM 394
287 ENTAFLTIVIDGULLPKAPAEIYEKKYXNMLPMWGINQOFCWIIIPMQLGYPLESEGKL 346
395 RKETITKMLMSTRLNLNITKEQVPLVVEYLDNNVHDHMKLRNMDIVODATFYATIL 454
347 DQKTATELLWKSYPINNVSKELTPVATEKYLGGTDDPVKK--KDLFLDMLADLLFGVPSV 404
455 QTAHYHEDAGLPVYLYFEHH-ARGIIVKPRTDGADGDEMDFLFGGPPFATGLSMGKKA 513
405 NVASHHRDAGAPTYMYEYRPSFSSDMRPRTVIGHGDEIFSVLGAPFLKEGATEEIK 464
514 LSLQMKYWANFARTGNPDGNLPCWPRYKNKDKYLQLDFTTRVGMKLEKQKQAFWMSLY 573
465 LSKVMKYWANFARNGNENGEGLPQWPAYDKYKGLQIGATTQAAQKLDKQKVAFAFTELW 524
574 --QSORPEK 580
525 AKEAAPRE 533

RESULT 12
EST1_MESAU STANDARD; PRT; 561 AA.
AC Q64419;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase precursor (EC 3.1.1.1).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN 1;
SEQUENCE FROM N.A.
RC STRAIN-Syrian golden; TISSUE=Liver;
RX MEDLINE=94318665; PubMed=8043605; Wang C.Y.;
RA Sone T., Isobe M., Takabatake E.;
RT "Cloning and sequence analysis of a hamster liver cDNA encoding a
RT novel putative carboxylesterase."
RL Biochim. Biophys. Acta 1207:138-142 (1994).
CC -1- FUNCTION: Involved in the detoxification of xenobiotics and in
CC the activation of ester and amide prodrugs.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D28566; BAA05913.1; --
CC PIR; S47655; S47655.
CC HSSP; P37967; 1QE3.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000379; Ser. esters.
CC Pfam; PF00135; Coesterase; 1.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

```

DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
 FT SIGNAL 1 27
 FT CHAIN 28 561
 FT ACT_SITE 227 227
 FT ACT_SITE 459 459
 FT DISULFID 95 122
 FT DISULFID 280 291
 FT SITE 558 561
 FT CARBOHYD 276 276
 FT CARBOHYD 362 362
 SQ SEQUENCE 561 AA; 62330 MW; 48EAL1E42475321 CRC64;

Query Match
 Best Local Similarity 34.18; Score 1060; DB 1; Length 561;
 Matches 234; Conservative 97; Mismatches 191; Indels 48; Gaps 14;

Qy 29 CWSLTCLMAQTALGALH--TKRPQVTKYGLQGMHV--GKTPIQVFLGVPSRPP 83
 Db 8 CWRVAVACGLLLLVHVGQDSVSPINHTGQVRGKLVYKGVTVGVAFLGIPAKPP 67
 Qy 84 LGILRFAPPPPPKGIKATATYPPGCLQESW--GQLASMYVSTRER---YKWLRFESD 138
 Db 68 VGFLRFAPPPPPKGIKATATYPPGCLQESW--GQLASMYVSTRER---YKWLRFESD 121
 Qy 139 CLYLVNVPARAPGDPOLPVWVFPFGAFTVGAASSVEGSDLAAREKVLVLELQHLGTF 198
 Db 122 CLYLVNVPARAPGDPOLPVWVFPFGAFTVGAASSVEGSDLAAREKVLVLELQHLGTF 181
 Qy 199 GFISTDSDHARGNGLLDQMAALRWQENIAAEGDPGNVTLFGQSAGAMISGLMMSP 258
 Db 182 GFISTDSDHARGNGLLDQMAALRWQENIAAEGDPGNVTLFGQSAGAMISGLMMSP 241
 Qy 259 ASGLFHAISQSTALFRLTITSNFLKVA--AKVAHLAGNHNSTQILVNCRLALSGTKVM 317
 Db 242 SKGLFHAISQSTALFRLTITSNFLKVA--AKVAHLAGNHNSTQILVNCRLALSGTKVM 301
 Qy 318 RVSNKMFQLNFORDEPIIWSNP--VVDGVVIPPDPVLLAQGVSSVYVLLGVNMLE 376
 Db 302 AINQ-----VFINTPGVVDGIFLRHPQELLASVDVFPVPSIIGVDSDE 345
 Qy 377 FNWLLPYMKFPLNQMRKETTITKMLWSTRLTNITKEQVPLVVEYLDNVNEHWKML 436
 Db 346 CGMGPVLFMGDLHVKNITRETLPAFLKRAEIMMLPPECSDILMLQYMGDV--EDPQTL 403
 Qy 437 RNRNMDIVQDATFYATLQTAHYHRDAGLPVLYEPEHARGI---IVKPRTDGADHDE 493
 Db 404 QACFRELKDFMFVLPALKVAYQQR--SHAPVYFEFQHQSFINKXDAPSHVRADEGH 462
 Qy 494 MYELFGPPFATGLSMG---KEKALSQMKYKWFANFARTGNPDGNLPCWPRYKNKDKYLQ 550
 Db 463 VAFVFGSDF--WGLKIDLTBEKLNKRMKYKWFANFARHGNPNSEGLPYNPDELVHDDQYLK 521
 Qy 551 LDFTRVGMKLEKKKAFWMSLVQSQRPEK 580
 Db 522 LDIQPAVGRAKSKKLFHWKIL-----PQK 547

RESULT 13

ESTM_MOUSE

ID_ESTM_MOUSE STANDARD; PRT; 554 AA.

AC Q6380;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Liver carboxylesterase precursor (EC 3.1.1.1) (ES-Male) (Esterase-31).

GN ES31.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=BAUB/CJ X DBA/2J; TISSUE=Liver;
 RX MEDLINE=93326638; PubMed=7916639;
 RA Aida K., Moore R., Negishi M.;
 RT "Cloning and nucleotide sequence of a novel, male-predominant
 RT carboxylesterase in mouse liver";
 RL Biochim. Biophys. Acta 1174:72-74 (1993).
 CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
 CC activation of ester and amide prodrugs.
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
 CC reticulum.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S64130; AAB27606.1; -;
 DR PIR; S34607; S34607.
 DR HSP; P37967; 1QB3.
 DR MGD; MGI:102773; Es31.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
 KW Signal; Multigene family.
 FT SIGNAL 1 14
 FT CHAIN 15 554
 FT ACT_SITE 215 215
 FT ACT_SITE 443 443
 FT DISULFID 83 110
 FT DISULFID 267 278
 FT SITE 551 554
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 381 381
 SQ SEQUENCE 554 AA; 61509 MW; 028D98B06F3CAAD CRC64;

Query Match
 Best Local Similarity 33.2%; Score 1034; DB 1; Length 554;
 Matches 232; Conservative 89; Mismatches 205; Indels 38; Gaps 9;

Qy 34 LCLMAQTALGALHTKRPQVTKYGLQGMHVGVKTP--IQVFLGVPSRPPILRFPAP 91
 Db 5 LLIFPTTVIGPKVT--QPEVDTPLGRVGRQGVKDTDRMNVNVLGIPPAQAPLGLRPSA 63
 Qy 92 PEPPEPWKIGIRDATYPPGCLQESWGQLASMYVSTRERYKWLRFESDCLYLVNVPARAP 151
 Db 64 PLPQPQWEGVGDASINPPMCLQDV--ERNMSRFTLINEKQKIFPISDCLTUNISPTBIT 122
 Qy 152 GDPQLPVNVPFPGGAFIVGAASSVEGSDLAAREKVLVFLQHLRIGIFGLSTDSDHARGN 211
 Db 123 AGDKRPVNVWTHGSLRVGSSTSHDGSALAAYGVVVTVQVRLGIFGLSTGDKHMPGN 182
 Qy 212 WGLLDQMAALRWQENIAAEGDPGNVTLFGQSAGAMISGLMMSPASGLFHAISQSG 271
 Db 183 RGFLDVAALRWQENIAAEGDPGNVTLFGQSAGAMISGLMMSPASGLFHAISQSG 242
 Qy 272 TALFRLTITSNPLKVAHVLAHAGNHNSTQILVNCRLALSGTKVMRVSNNKMFQLNLFQ 331
 Db 243 VVISKILSDLNWSEAFQNFANSVACGSAPAEVLQCLQKQEGKDLITKKNV----- 293
 Qy 332 RDPSEIIMSPVVDGVVIPPDLVLLTQGVKSSVYVLLGVNNEFNWLLPYIMKFPPLNR 391
 Db 294 -----NISYTVNDSFFPQPKLANKQFPTVYLLGVNTHFEFGWLL---LKFNNIL 342


```

CC 4/Beta 4B5B. Interacts with neuexin 2-beta isoforms 3/Beta 4B5A,
CC 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with
CC neuexin 3-beta. Probably interacts through its C-terminus with
CC DLG4/PSD-95 third PDZ domain (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q62888-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q62888-2; Sequence=VSP_007533;
CC -|- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal
CC root ganglion.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U41662; AAA97870.1; -
CC HSP; P37967; IQE3.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000460; Neuroligin.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PF00135; Coesterase; 1.
CC PROSITE; PS01090; NEUROLIGIN.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing
FT SIGNAL 1 14 PROBABLE.
FT CHAIN 15 836 NEUROLIGIN 2.
FT DOMAIN 15 678 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 679 699 POTENTIAL.
FT DOMAIN 700 836 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 141 BY SIMILARITY.
FT DISULFID 317 328 BY SIMILARITY.
FT DISULFID 487 521 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 153 169 Missing (in isoform 2).
FT FTId=VSP_007533.
SQ SEQUENCE 836 AA; 90961 MW; 1AD51CB1BE4BF9CF CRC64;
Query Match 27.3%; Score 849; DB 1; Length 836;
Best Local Similarity 33.2%; Pred. No. 1.3e-59;
Matches 215; Conservative 92; Mismatches 191; Indels 150; Gaps 21;
Qy 30 WSLTLCIM---AQ-----TALGALHTKR-PQVVKYKGLGKQMHVGKT 69
Db 2 WLLALCLVLGAGQGGGPGGAPGGGLGSLGEEFPVNTAYTAVRGVRELNNE 61
Qy 70 ---PIQVFLGVFSPPLGILRFAPPEPPEPWKGIKIDATTPPGCLQESWGOL----- 119
Db 62 ILGFWVQFLGVVATPPLGARRFPQPEAPASWPGVGNATTLPPACPNLHGALPAIMLPV 121
Qy 120 -----ASMVSTRERYKWLRFESDCLVINYAPAR-----APGDQL--- 156
Db 122 WFTDNLEAAATYVQNG-----SEDCLYLNLYVPTEDGPLTKKSDATLNPPTDIRD 173
Qy 157 ---PVMWVFPGGAFIVGAASSYEGSDLAAREKVLVFLQHRLGIFGFLSTDDSHARGNW 212
Db 174 SGKKPVMFLHGGSGYMEGTGMFDGSLAAYGNVIVATLNYRLGVLGFLSTGDAQAKGY 233
Qy 213 GLLDQVAALRWQENTIAAFGDPGNVTFLFQSGASAMISGLMMSPLASGLFHRATISQSGT 272
Db 234 GLLDQIQALRWLSNTIAHFGDPERITIFGSGAGASCVNLLILSHHSEGLFQKATAQSGT 293
Qy 273 ALFRLFTSPLKVAKVVAHLACGNHNSITQLVNCRLALSGTKVMVSNKMRFLQLNFOR 332

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Search completed: August 3, 2004, 22:28:20
Job time : 15 secs

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Db 294 AISSWSVNYQPLKYTRLLAAKVGCDREDSTEAVECLRRKSSREL-----VDQDV 342
Qy 333 DPBEIIMSVPVGVWIPDDPLVLLTQGGKVSVPYLLGVNNLB----- 376
Db 343 QPARYHIAFGVPVGDVVDPPDPEILMQGGEFLNVDMLIGVNOGEGLKFEVDSAESEGV 402
Qy 377 ---FNW-----LLPYIMKFPPLNRQAMRKETITKMLWSTRLTLNITKEQVPLVVEYLDNVN 429
Db 403 ASAFDFTVSNEFDNLYGYPEGKDVLR-ETIKFM-----YTDWAD 440
Qy 430 EHDKMLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYEPEHH--ARGIIVKPRTDG 487
Db 441 RDNGEMRKTLTLLFTDHWVAPAVATAKLHADYQSPVYFTFYHHQAEQ---RPEWAD 497
Qy 488 ADHGDENVYLFEGGPF--ATGL---SMGK-EKALSLOMKYKWANFARTGNPNNDGNLP---- 537
Db 498 AAHGDELPPYVFGVMVGATDLFPCNFSKNDVMLSAVVMTYWTNFAKTGDPNQ-PVPQDTK 556
Qy 538 -----CWPRYN-KDEKYLQDLFTTRVGKMLKEKGMATFMSL 572
Db 557 FIHTKPNRFEVWWSKFSKSKQYLHGLKPRVDRDNYRANKVAFWLEL 604

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OM protein - protein search, using sw model

Run on: August 3, 2004, 22:24:10 ; Search time 42 Seconds

(without alignments)
4387.205 Million cell updates/sec

Title: US-10-001-227-2

Perfect score: 3112

Sequence: 1 MFSTPLPSTVLPSSLPTAGA.....KMAFWSLVQSRPEKQRF 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2182.5	70.1	556	11 Q8ROW5	Q8ROW5 mus musculus
2	1930	62.0	367	4 Q8N9F4	Q8N9F4 homo sapien
3	1287.5	41.4	556	6 Q864S9	Q864S9 felis silve
4	1284	41.3	555	6 Q95N05	Q95N05 canis famil
5	1282	41.2	556	6 O46421	O46421 macaca fasc
6	1265	40.6	555	4 Q96EE8	Q96EE8 homo sapien
7	1264	40.6	555	4 Q8TDZ9	Q8TDZ9 homo sapien
8	1260	40.5	555	6 O77540	O77540 oryctolagus
9	1254	40.3	555	11 Q9R135	Q9R135 rattus norv
10	1252	40.2	565	11 Q91YG2	Q91YG2 rattus norv
11	1248.5	40.1	567	4 Q9UK77	Q9UK77 homo sapien
12	1247	40.1	555	11 Q35534	Q35534 mesocricetu
13	1244.5	40.0	555	11 Q91ZV9	Q91ZV9 mus musculu
14	1244.5	40.0	555	11 Q8VCT4	Q8VCT4 mus musculu
15	1242.5	39.9	555	11 Q924V8	Q924V8 mus musculu
16	1241	39.9	555	6 O97582	O97582 sus scrofa

17	1239	39.8	567	4 Q86UK2	Q86UK2 homo sapien
18	1235.5	39.4	567	4 Q8ULY1	Q8ULY1 homo sapien
19	1198.5	38.5	565	11 Q8VCC2	Q8VCC2 mus musculu
20	1196.5	38.4	565	11 Q55136	Q55136 mus musculu
21	1155	37.1	545	6 Q81O34	Q81O34 felis silve
22	1145.5	36.8	561	11 Q91WU0	Q91WU0 mus musculu
23	1140	36.6	565	11 P70104	P70104 cavia porce
24	1130.5	36.3	554	11 O54936	O54936 mus musculu
25	1130.5	36.3	554	11 Q8K125	Q8K125 mus musculu
26	1122	36.1	559	11 Q35533	Q35533 mesocricetu
27	1116	35.9	562	11 Q924V9	Q924V9 rattus norv
28	1100	35.3	560	11 Q8R097	Q8R097 mus musculu
29	1083	34.8	559	4 Q00748	Q00748 homo sapien
30	1083	34.8	623	4 Q81UP4	Q81UP4 homo sapien
31	1079.5	34.7	561	11 Q70177	Q70177 rattus norv
32	1068	34.3	554	11 Q35535	Q35535 rattus norv
33	1067.5	34.3	568	4 Q726U1	Q726U1 homo sapien
34	1063	34.2	572	11 Q810S9	Q810S9 mus musculu
35	1058.5	34.0	558	11 Q8K3R0	Q8K3R0 rattus norv
36	1057	34.0	559	11 Q8BK48	Q8BK48 mus musculu
37	1053.5	33.9	558	11 Q80ZR3	Q80ZR3 mus musculu
38	1053.5	33.9	561	11 Q91WGO	Q91WGO mus musculu
39	1051.5	33.8	568	11 Q8VCU1	Q8VCU1 mus musculu
40	1047	33.6	559	11 Q8BM97	Q8BM97 mus musculu
41	1045	33.6	607	4 Q81CP8	Q81CP8 homo sapien
42	1044	33.5	607	4 Q7Z366	Q7Z366 homo sapien
43	1024	32.9	525	4 Q96DN9	Q96DN9 homo sapien
44	1021.5	32.8	561	11 Q70631	Q70631 rattus norv
45	956	30.7	469	4 Q8NBC8	Q8NBC8 homo sapien

ALIGNMENTS

RESULT 1

Q8ROW5 PRELIMINARY; PRT; 556 AA.
AC Q8ROW5;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN BC026374.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; BC026374; AAH26374.1; -.
DR MGI; MGI:2384581; BC026374.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 556 AA; 62122 MW; EB31F4F34990446 CRC64;

Query Match	70.1%;	Score 2182.5;	DB 11;	Length 556;
Best Local Similarity	71.8%;	Pred. No. 5.5e-177;		
Matches 400;	Conservative 68;	Mismatches 86;	Indels 3;	Gaps 3;
QY	24	NRWICWLSLTCLMAQTALGALHTKRPQVVTKYGTLOGKQHWGKTQIQLVGFVPSRPP	83	
Db	1	MKWILGLSLTCLVQVQALGALHTKEPLITKHGILQKQVHVGDTPQVFLGIFPSKPP	60	
QY	84	LGILRFAPPEPPEPWKIGIRDATTTPPGCLQBSWQLASMYVSTRERYKNLRFSEDCLYLN	143	

Db 61 VGTERRAPPBPPLPWNGIRDATTYPSCLQESWGQILSMYLNTRKQYKWLHSESDCLYN 120
 QY 144 VYAPARAPGDPQLPVMWPPGGAFTVGAASSYEGSDLAAREKVLVFLQHRIGIFGFLST 203
 Db 121 VYAPVLAPGAPLPLPVMWPPGGAFTVGAASSYEGSDLAAREKVLVFLQHRIGIFGFLST 180
 QY 204 DDHARGNGLLDQMAALRWQENIAAFGDPGNVTLFGQSAGAMSISGLMWSPLASGLF 263
 Db 181 GNSHARGNGLLDQMAALRWQENIAAFGDPGNVTLFGQSAGAMSISGLMWSPLASGLF 240
 QY 264 HRAISQGTALFLFTTSNPLKVAHLAGCNHNSTQILVNCRLSALSGTKVMRVSNNKM 323
 Db 241 HQAISQGTAVLKAFITPPLTSNPLKVAHLAGCNHNSTQILVNCRLSALSGTKVMRVSNNKM 300
 QY 324 REQLNFORPDEI IWSMSPVVDGVI PDDPLVLTQGVSSVYLLGVNNLEFVWLLPY 383
 Db 301 SFTQASHDKDKEIVFLSPVVDGVI PDDPLVLTQGVSSVYLLGVNNLEFVWLLPY 360
 QY 384 IMKFPNLRQARKETITKMLWSTRTLLNITKEQVPLVVEEYL-DNVNEDHDKMLNRNMD 442
 Db 361 LMKIQLNORMNQTINKILWSTRTLLNITKEQVPLVVEEYL-DNVNEDHDKMLNRNMD 420
 QY 443 IVODATFVYATLQATYHRDAGIPVLYEYFEHHA-RGIIVKPTDGDHGDGDEMFLGFP 501
 Db 421 LGDATFVYATLQATYHRDAGIPVLYEYFEHHA-RGIIVKPTDGDHGDGDEMFLGFP 479
 QY 502 FATGLSMGKEKALSLOWMYKWNFASTGNPNDGNLPCWPRYNKDEKYLQDFTTRVGMKL 561
 Db 480 FSKGSAGKEKFSLOWMYKWNFASTGNPNDGNLPCWPRYNKDEKYLQDFTTRVGMKL 539
 QY 562 KEKMAFWWSLYOSQRP 578
 Db 540 KEKMAFWWSLYOSQRP 556

RESULT 2

Q8N9F4 PRELIMINARY; PRT; 367 AA.
 AC Q8N9F4;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ37464.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
 RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
 RA Irie R., Osuki T., Sato H., Oka T., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kikuchi H., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
 RA Takahashi-Fujii A., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
 RA Sugano S., Nagahari K., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA "NEDO human cDNA sequencing project."
 RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; AK094783; BC04422.1;
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 KW Hypothetical protein; Hydrolase.
 SQ SEQUENCE 367 AA; 41851 MW; 95671668E6F2FA7C CRC64;

Query Match 62.0%; Score 1930; DB 4; Length 367;
 Best Local Similarity 99.7%; Pred. No. 9.3e-156;

Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 218 MAALRWQENIAAFGDPGNVTLFGQSAGAMSISGLMWSPLASGLPHRAISQGTALFRL 277
 Db 1 MAALRWQENIAAFGDPGNVTLFGQSAGAMSISGLMWSPLASGLPHRAISQGTALFRL 60
 QY 278 FITSNPLKVAHLAGCNHNSTQILVNCRLSALSGTKVMRVSNNKRFQLNFORPDEI 337
 Db 61 FITSNPLKVAHLAGCNHNSTQILVNCRLSALSGTKVMRVSNNKRFQLNFORPDEI 120
 QY 338 IWSMSPVVDGVI PDDPLVLTQGVSSVYLLGVNNLEFVWLLPYIMKFPNLRQARK 397
 Db 121 IWSMSPVVDGVI PDDPLVLTQGVSSVYLLGVNNLEFVWLLPYIMKFPNLRQARK 180
 QY 398 TITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEDHDKMLNRNMDIVQDATFYATLQTA 457
 Db 181 TITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEDHDKMLNRNMDIVQDATFYATLQTA 240
 QY 458 HYHRDAGLPVLYEYFEHHA-RGIIVKPTDGDHGDGDEMFLGFPFATGLSMGKEKALSQ 517
 Db 241 HYHRDAGLPVLYEYFEHHA-RGIIVKPTDGDHGDGDEMFLGFPFATGLSMGKEKALSQ 300
 QY 518 MYKWNFASTGNPNDGNLPCWPRYNKDEKYLQDFTTRVGMKLKEKMAFWWSLYOSOR 577
 Db 301 MYKWNFASTGNPNDGNLPCWPRYNKDEKYLQDFTTRVGMKLKEKMAFWWSLYOSOR 360
 QY 578 PEKQRF 584
 Db 361 PEKQRF 367

RESULT 3

Q864S9 PRELIMINARY; PRT; 566 AA.
 AC Q864S9;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Carboxylesterase.
 GN CCSI.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Miyazaki M., Sai H., Taira H., Yamashita T.;
 RT "Molecular cloning of the feline liver carboxylesterase."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB094147; BAC75712.1;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00141; CARBOXYLESTERASE_B_2; 1.
 SQ SEQUENCE 566 AA; 62231 MW; 4677D3F67205AD53 CRC64;

Query Match 41.4%; Score 1287.5; DB 6; Length 566;
 Best Local Similarity 45.7%; Pred. No. 9.6e-101;
 Matches 252; Conservative 107; Mismatches 184; Indels 9; Gaps 6;

QY 26 WILCWSLITCLMAQTALGALHTKRPQV-TKYGTLOGKQMHVG--KTQVFLGVFPSPR 82
 Db 2 WILCWSLITCLMAQTALGALHTKRPQV-TKYGTLOGKQMHVG--KTQVFLGVFPSPR 59
 QY 83 PLGILRAPPEPPEPWKIGIRDTATYPPGCLQE-SMGQLASMYVSTERYKWLRFSEDCLY 141
 Db 60 PLGILRAPPEPPEPWKIGIRDTATYPPGCLQE-SMGQLASMYVSTERYKWLRFSEDCLY 119
 QY 142 LNVYAPARAGDPQLPVMWPPGGAFTVGAASSYEGSDLAAREKVLVFLQHRIGIFGFL 201


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QY 36 LMACTALGALHTKRPQV-TKYGTLOGQMHV-GKT-PQVGLGVFSPSPPLGILRRAPP 92
Db 11 LALFTAWG--HPSPPPVVDVHGKVLGKFSLEGGTQPVAVFLGIFPAKPPGURFTFP 68
QY 93 EPPEPMKGIKDATYPPGCLQES-WGQLASMYSTRERYKWLRFSDCLYLNVYAPARAP 151
Db 69 QPAEPKSFVNKATSYPPMCSQDAVAGVLSLFTNKKENTPLKLSLSDCLYLNIYTPADLT 128
QY 152 GDFQLPVMWFPFGATVGAASSYEGSDLAAREKVLVFLQRLGIFGLSTDDSHARGN 211
Db 129 KQRLPVMWIHGGGLVWGAASYDGLAALAHENVVVVTIOVRLGIWGFSTGDEHSRGN 188
QY 212 WGLDDMAALRWQENIAAFGGDPGNVTLFGQAGAMSISGLMMSPLASGLFHRALISQSG 271
Db 189 WGHLDQLAALRWQDNIAASFGNPGSVTIFGESAGGESVSLVSLAKNLFHRALISG 248
QY 272 TALFRFITSNPLK-VAKKVAHLACGNHNSQTILVNCRLALSGTKVMRVSNKORFLQINF 330
Db 249 VALTAVLVKKGDKPLAEQIAAAGCQTITTSAMVHCLRQKTEEBELTTLKMKFFSLDL 308
QY 331 QRPDEEIIWMSMPVWDGWIPIIDPLVLLTQGVSSVYLLGVNLFENLPLVIMKFFPLN 390
Db 309 HGDPDRSHPLGTVIDGLLPKTPPELOARKEKNTVPVWGNKQFEGHIIPLMKGYPIS 368
QY 391 RQAMRKETITKMLWSTRTLNITKEQVPLVVEYLDNVNHEHDKMLRNRMMDIVQDATFV 450
Db 369 EGKLDQKTAMSLWKSVPLVYIAKELIPBATEKYLGGTDDPVKK--KDRFLDOLLADVWFS 426
QY 451 YATLOAHVHRDAGLPVLYEFPHH-ARGIIIVKPRTDGADHGDGMYFLFGGSPATGLSNG 509
Db 427 VPSVIVARHHRDAGVPTMYEFOYRFSFSDMKPKTVIGDHGDELFSVFGAPFLKEGASE 486
QY 510 KEKALSQMKMYWANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGMKLEKXKMAFW 569
Db 487 EEIRLSQWYKFWANFARNNGNPNGEGLPRWPEYNQEEYLIQICANTQAAQKLKDEKVAFW 546
QY 570 MSILYQSORPEKQKQ 583
Db 547 TTLFAKKAVERKPPQ 560

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RESULT 6

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Q96EE8 PRELIMINARY; PRT; 566 AA.
ID Q96EE8 AC Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Lung;
RC Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; BC012418; AH12418.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase_1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Hypothetical protein; Hydrolase.
SQ SEQUENCE 566 AA; 62269 MW; 3B86CBA1C42BAA0F CRC64;

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Query Match 40.6%; Score 1265; DB 4; Length 566;
 Best Local Similarity 43.2%; Pred. No. 7.9e-99;
 Matches 252; Conservative 111; Mismatches 189; Indels 32; Gaps 8;

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QY 6 LPSTVLSLLPTAGAGSMEMWILCWSLITCLMAQTALGALHTKRPQV-TKYGTLOGK-- 62
Db 3 LPAULVATL--ASAANG-----HPSPPPVVDVHGKVLGKFSLEGGTQPVAVFLGIFPAKPPGURFTFP 38
QY 63 QMHVGKTIQVFLGVFSPSPPLGILRPAPEPEPMKGIKDATYPPGCLQES-SWGLQAS 121
Db 39 SLEGFAQVAFILGIPPAKPPGLPLRFTPPQAPAPMSFVNKATSYPPMCTQDPAKAGLLS 98
QY 122 MYVSTRERYKWLRFSDCLYLNVYAPARAGDQLPVMWFPFGATVGAASSYEGSDLA 191
Db 99 ELFNKRIENPLKLSLSDCLYLNIYTPADLTCKRLPVMWIHGGGLVWGAASYDGLALA 158
QY 182 AREKWLIVFQHRIGIFGLSTDDSHARGNWLGLDDMAALRWQENIAAFGGDPGNVTLF 241
Db 159 AHENVVVVTIOVRLGIWGFSTGDEHSRGNWGHLDQVLAALRWQDNIAASFGNPGSVTIF 218
QY 242 QOSAGAMSISGLMMSPLASGLFHRALISQSGTALFRFITSNPLK-VAKKVAHLACGNHNS 300
Db 219 GESAGGESVSLVSLAKNLFHRALISGVALTSVLVKKGDYKPLAEQIAITAGCKTTT 278
QY 301 TQILVNCRLALSGTKVMRVSNKORFLQINFQRPDEEIIWMSMPVWDGWIPIIDPLVLLTQ 360
Db 279 SAVNVHCLRQKTEEBELTTLKMKFFSLDLOGDPRESQPLGTVIDGMLLLKTPELQAE 338
QY 361 GKVSYPYLLGVNLFENLPLVIMKFFPLNRMQAMRKETITKMLWSTRTLNITKEQVPLV 420
Db 339 RNHTVPMVGVINKQEFGLIPMLMSYPLSEGQDKTAMSLWKSVPLVYIAKELIPEA 398
QY 421 VEEILDNVNHEHDKMLRNRMMDIVQDATFVYATLOAHVHRDAGLPVLYEFPHH-ARGI 479
Db 399 TEKLYGTD--DVTKKKDLFDLIADVMFGVPSVIVARHHRDAGAPTYMEFOYRFSFSS 456
QY 480 IVKPRTDGADHGDGMYFLFGGSPATGLSNGKEKALSQMKMYWANFARTGNPDGNLPCW 539
Db 457 DMKPKTVIGDHGDELFSVFGAPFLKEGASEEIRLSQWYKFWANFARNNGNPNGEGLPHW 516
QY 540 PRYNKDEKYLQDFTTRVGMKLEKXKMAFWMSILYQSORPEKQKQ 583
Db 517 PEYNQKEGYLIQICANTQAAQKLKDEKVAFWTTLFAKKAVERKPPQ 560

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RESULT 7

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Q8TD29 PRELIMINARY; PRT; 565 AA.
ID Q8TD29 AC Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29 Q8TD29
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Brain carboxylesterase hBr2.
GN CES HBR2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Hosokawa M., Mori M., Ogasawara Y., Komori C., Tsukada E., Chiba K.;
RT "cDNA cloning and expression of carboxylesterase isozymes from human brain.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mori M., Hosokawa M., Tsukada E., Ogasawara Y., Chiba K.;
RT "cDNA cloning and stable expression of human brain carboxylesterase isozymes.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB025027; BAB85656.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.

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DR	InterPro: IPR000379; Ser_estrs.	DR	Pfam: PF00135; Coesterase; 1.	DR	PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.	DR	PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.	KW	Hydrolase.	QY	SEQUENCE 565 AA; 61962 NW; E255244C2CA9A1AE CRC64;																																																																																														
QY	26	WILWLSLTCLMAQTALGALHTKRPQVVKYGTGQKHQHVGV--KTIPIQVFLGVFPSPRRP 83	Db	2	WL--FDLVLTSLATSWANGYSLPVPDVTQGVKLVGKVSLEGFAQPVAVFLGVPPAKP 59	QY	84	LGLRPAPEPPKNGIRDATTTPPGCLQES--WGQLASMYVSTRRYKWLRFSEDCILY 142	Db	60	LGLRPAFPQAAPNPNFKNTTTPPMQSGDAVGGVLSLFTNRKDNPLRFSEDCILY 119	QY	143	NYVAPARAPDQPLPMWVFGGAFIVGAASVEGSDLAAREKVLVFLQHLRGLTGFPLS 202	Db	120	NIYTPADLTKNRGLPMWVIIGGGLVVGCASTYDGLALSAHENVVVVYQYRLGIWGFPS 179	QY	203	TDSDHARGNWGLDDMAALRWQENIAAFGDDPQNVTLFGQSAGAMSISGLMMSPLASGL 262	Db	180	TGDEHGRGNWGHLDQALALRWQENIANFNGNPGSVTIFGESAGGSSVVLVLSPLAKNL 239	QY	263	FHRATSSQGTALFRLFITSNPLKVAKKVAHLAGCNHNSTOILVNCLEALSCTKWVRVSNK 322	Db	240	FHRATSESGVALTAALVKDKMKDTAQIATVAGCKSTTSAVLVHCLURQKTEDELLEVSLK 299	QY	323	MRFLQLNFORDEEETIWSNPSVVDGWIIPDDPLVLLTQGVKSSVPVLLGVNNLEFNWLLP 382	Db	300	LKEFTLLDGLDPRSYPVPLPTVVDGVLVLPKMPQILAEKKFNFSVPYIIGIKQEFGLWLLP 359	QY	383	YIMKPLNFAQMKETITIKMLWSTFTLNIYKEQVPLVVEYLDNVNHDWMLRNMMD 442	Db	360	MMWGYPLSDKLDQKTASSLLMKSYPIANIPEELTPLASEKYLGGTDDDPVKK--KALFLD 417	QY	443	IVQDAFVYATLTQAHYHRDAGLPPVLYEFEPHH--ARGIIVKPRTDGADHDEMYPFLGGP 501	Db	418	MLGDDVFGVSPVTVAHRHDAGAPYIMYEFQYHFSFSDMKKQPTVVDGHDGDELFSVFGAP 477	QY	502	FATGLSMGKEKALSLOMKMYWANFARTGNPDGNLPCWPRYNKDEKYLQDLFTTRVGMKL 561	Db	478	FLKGGASBEIRLSKMMKMLWANFARSCNPMGKGCSSWPAYDQEGYQLIGIPTQAQKL 537	QY	562	KEKKMAFWMSLYQSQRPEK 580	Db	538	KSKEMAFWTELLAKGAAEK 556	RESULT 8	O77540	PRELIMINARY; PRT; 565 AA.	ID	O77540	PRELIMINARY; PRT; 565 AA.	AC	O77540	PRELIMINARY; PRT; 565 AA.	DT	01-NOV-1998	(TEMSLurel. 08, Created)	DT	01-NOV-1998	(TEMSLurel. 08, Last sequence update)	DT	01-OCT-2003	(TEMSLurel. 25, Last annotation update)	DB	Liver catboxylesterase (EC 3.1.1.1).	OS	Oryctolagus cuniculus (Rabbit).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	OX	NCBI_Taxid=9986;	RP	[1]	RP	SEQUENCE FROM N.A.	RC	TISSUE=Liver;	RC	MEDLINE=98257515; PubMed=9635592;	RX	Potter P.M., Pawlik C.A., Morton C.L., Naeve C.W., Danks M.K.;	RA	"Isolation and partial characterization of a cDNA encoding a rabbit	RT	liver catboxylesterase that activates the prodrug irinotecan (CPT-	RT	11).";	RL	Cancer Res. 58:2645-2651(1998).

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CC  -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR  EMBL; AF036930; AAC39258.1; -.
DR  PDB; 1K4Y; 01-MAY-02.
DR  GO; GO:0016787; F:hydrolase activity; IEA.
DR  GO; GO:0004759; F:serine esterase activity; IEA.
DR  InterPro; IPR002018; CarbesteraseB.
DR  InterPro; IPR000379; Ser_estrs.
DR  Pfam; PF00135; Coesterase_1.
DR  PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR  PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR  Hydrolase.
SQ  SEQUENCE 565 AA; 62291 MW; 0ACDG61400CC81D2F CRC64;

Query Match 40.5%; Score 1260; DB 6; Length 565;
Best Local Similarity 43.8%; Pred No. 2.1e-98;
Matches 245; Conservative 113; Mismatches 180; Indels 16; Gaps 9;

Qy 34 LCLMAQTALGAL----HTKSPQVV--TKYGTLOGK--QMHVGTKPIQVFLGVPSFRPPLGI 86
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 LCALLASLAACATAGWHPSPAPPVVDTVHGKVLGKFSVLEGFAQVAVFLGVPPFAKPPLGS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 87 LRAPPPEPPFWKIGIRDATTPGCCLOE--SWGOLASMYVSTERYKWLRFSEDCLYLVN 144
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 LRAPPQAPASWSHWKNTTTPYPCMSODAVSGHMLSEFTNRKENIP-LKFSEDCLYINI 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 145 YAPARAPGDPQLPFWVWFFPGARTVGAASYEGSDLAAREKVLVLFQHRLIGIEFLSTD 204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 YTPADLTKRGLPFWVWIHGGLMVGASTYDGLALSAHENVVVVTVQYRLGIWGFSTG 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 205 DSHARGNWGLLDQWAALRWQENIAARGGDPGNVTLFGQSAGAMSISGLXMSPLASGLFH 264
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 DEHSRGNWGHLDQWAALRWQDNIAFGGPGSVTFEGSAGGQSVILLLSPLTKNLFH 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 265 RAISOSGTALFRLLFTSNPLKVAKKVAHLACGNHNSTQILVNCRLRSLSGTKMVRVSNKVR 324
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 RAISESGVALLSFLFRKNTSLAEKIALI EAGKTTTSAMVHVCLRKQTEBELMEVTLKWK 301
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 325 FLQNFORDPEEIIWMSPPVDGVVDPDDLVLVLTQKVSVPVLLGVNNLEFNWLLP-Y 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 FMAULDVGDPKNTAFATTTVDGVLKPAAEILAEKYNMLPYVVGINQOEFGWIIIPMQ 361
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 384 IMKPEPLNRQMRKETITKMLKSTETLNIATKEQVPLVVEEYLDVNNVHDMKLRNVMDI 443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 MLGVPPLSEGKLDQKTATELLWKSPYVNVSKELTPVATEKYLGGTDDPVKK--KDLFLDM 419
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 444 VQDATFYVYATQTAHYHRDAGLPVLYEFEHH--ARGIIVKPRTPDGAHDGDMYFLFGPFF 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 LADLLFGVPSVNVARHRDAGAPTYMEYRYRPSFSDMRPKTVIGHGDEIFSVLGAPF 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 503 ATGUSMGEKALSQMKYWANFARTGNPDGNLPCWRYNKDEKYLQDLETTTVGMKKLK 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 LKEGATEETETKLSXNVKYWANFARNNGEGULPQWPAYDYKEGYLQIGAITTAAQKLK 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 563 EKKVAFWMSLY--QSORPEK 580
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 540 DKEVAFWTELWAKEAARPRE 559
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
ID Q9R135 PRELIMINARY; PRT; 565 AA.
AC Q9R135;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Carboxylesterase (EC 3.1.1.1) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;

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RA Ryu J.W., Lee W., Jung C.Y.;
 RT "Rattus norvegicus adipocyte carboxylesterase mRNA";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBCP databases.
 CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; AF171640; AA049369.1; -.
 DR PIR; A45140; A45140.
 DR PIR; S10367; S10367.
 DR HSSP; P21836; IMAA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004759; F:serine esterase activity; IEA.
 DR InterPro; IPR000318; CarbesteraseB.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 FT NON TER.
 SQ SEQUENCE 565 AA; 62130 MW; FDDBL9F2C5DD4ECO CRC64;
 Query Match 40.3%; Score 1254; DB 11; Length 565;
 Best Local Similarity 42.8%; Pred. No. 6.8e-98;
 Matches 240; Conservative 120; Mismatches 183; Indels 18; Gaps 6;
 QY 28 LCWSLTCLMAQTALG-----ALHTKRPQVTKYGTLOGKQMHVGTPIQVFLGVPPSR 81
 DB 6 LWM---LFLAATAWGYFSPPPVNTVKGLGKYVNLGFAQ-----PVAVFLGIPFAK 57
 QY 82 PPLGILRFAPPEPEPPKGIKRDATTYPGCLQES-WGQLASMYVSTRERYKMLRFSEDC 140
 DB 58 PPLGSLRFAPQPAEPNFKNTTSYPPMCSQDVGQVLSLFTNRKENIPLQFSEDC 117
 QY 141 YLNYAPARAGDPQLPVMWFFGGAPFVGAASYPGSDLAAREKVVLQVLRIGIF 200
 DB 118 YLNYTPADLTQKSLRFVWMIHGGVLVGGASTYDQVLSAHENVVVVTIQYRLG 177
 QY 201 LSTDDSHARGNWGLDQMAALRWQENIAAFGDPGNVTLFGOSAGMSISGLMWSPLAS 260
 DB 178 FSTGDEHSRGNWGLDQVAALHWQDNIANFNGNPGSVTFGESAGFSVALVSLAK 237
 QY 261 GLFHRAISQGTALFRFLITSNPLKVAKVLAHAGCNHNSITLVNCLRALSGTKMVRVS 320
 DB 238 NLFHRAISESGVLTSLALITDSKPIANLIATLSGCKTTTSAVMVHCLRQKTEDELETS 297
 QY 321 NKRFQLNFORPBEILINSMSPVWGVIPDDPLVLLTQGVSSVPYLLGVNLEFNWL 380
 DB 298 LKLNLFKDLGLGNPKESYPFLPTVIDGVLPKTPPEILAEKSFNTVPYIVGINKQEF 357
 QY 441 MDIVQDATFYATLOTAAHVRDAGLPVLYVEFEHARGI-IVKPRTDGADHDEMFLFG 499
 DB 416 QDLVADVIFGVPSVMVSRSHRDAGAPTFYEFYRPSFVSAMRPKTVIGHGDELFSVFG 475
 QY 500 GPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGM 559
 DB 476 SPFLKDGASEEETNLSKMWKYWANFARNGSPNGGLPHWPEYDQKEGKLGASTQAAQ 535
 QY 560 KLKEKQAFWMSLYQSOREK 580
 DB 536 RLKXKEVAFWSELRAKEAAEE 556
 RESULT 10
 QY1Y2 PRELIMINARY; PRT; 565 AA.
 AC QY1Y2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Carboxylic ester hydrolase (EC 3.1.1.1).
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_taxid=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;
 RX MEDLINE=21413896; PubMed=11429416;
 RA Wallace T.J., Kodsi E.M., Langston T.B., Grogan W.M.;
 RT "Mutation of Residues 423 (Met/Ile), 444 (Thr/Met), and 506 (Asn/Ser)
 RT Confer Cholesteryl Esterase Activity on Rat Lung Carboxylesterase.";
 RT SER-506 IS REQUIRED FOR ACTIVATION BY CAMP-DEPENDENT PROTEIN KINASE.";
 RL J. Biol. Chem. 276:33165-33174 (2001).
 CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; L81144; AAL00849.1; -.
 DR PIR; A45140; A45140.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004759; F:serine esterase activity; IEA.
 DR InterPro; IPR000318; CarbesteraseB.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 565 AA; 62117 MW; F3294B66AD2141BD CRC64;
 Query Match 40.2%; Score 1252; DB 11; Length 565;
 Best Local Similarity 42.8%; Pred. No. 1e-97;
 Matches 240; Conservative 119; Mismatches 184; Indels 18; Gaps 6;
 QY 28 LCWSLTCLMAQTALG-----ALHTKRPQVTKYGTLOGKQMHVGTPIQVFLGVPPSR 81
 DB 6 LWM---LFLAATAWGYFSPPPVNTVKGLGKYVNLGFAQ-----PVAVFLGIPFAK 57
 QY 82 PPLGILRFAPPEPEPPKGIKRDATTYPGCLQES-WGQLASMYVSTRERYKMLRFSEDC 140
 DB 58 PPLGSLRFAPQPAEPNFKNTTSYPPMCSQDVGQVLSLFTNRKENIPLQFSEDC 117
 QY 141 YLNYAPARAGDPQLPVMWFFGGAPFVGAASYPGSDLAAREKVVLQVLRIGIF 200
 DB 118 YLNYTPADLTQKSLRFVWMIHGGVLVGGASTYDQVLSAHENVVVVTIQYRLG 177
 QY 201 LSTDDSHARGNWGLDQMAALRWQENIAAFGDPGNVTLFGOSAGMSISGLMWSPLAS 260
 DB 178 FSTGDEHSRGNWGLDQVAALHWQDNIANFNGNPGSVTFGESAGFSVALVSLAK 237
 QY 261 GLFHRAISQGTALFRFLITSNPLKVAKVLAHAGCNHNSITLVNCLRALSGTKMVRVS 320
 DB 238 NLFHRAISESGVLTSLALITDSKPIANLIATLSGCKTTTSAVMVHCLRQKTEDELETS 297
 QY 321 NKRFQLNFORPBEILINSMSPVWGVIPDDPLVLLTQGVSSVPYLLGVNLEFNWL 380
 DB 298 LKLNLFKDLGLGNPKESYPFLPTVIDGVLPKTPPEILAEKSFNTVPYIVGINKQEF 357
 QY 441 MDIVQDATFYATLOTAAHVRDAGLPVLYVEFEHARGI-IVKPRTDGADHDEMFLFG 499
 DB 416 QDLVADVIFGVPSVMVSRSHRDAGAPTFYEFYRPSFVSAMRPKTVIGHGDELFSVFG 475
 QY 500 GPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGM 559
 DB 476 SPFLKDGASEEETNLSKMWKYWANFARNGSPNGGLPHWPEYDQKEGKLGASTQAAQ 535
 QY 560 KLKEKQAFWMSLYQSOREK 580
 DB 536 RLKXKEVAFWSELRAKEAAEE 556
 RESULT 11
 QYUK77 PRELIMINARY; PRT; 567 AA.
 ID QYUK77


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AC Q9UK77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Egsyn.
OS Homo sapiens (Human)
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Islam M.R., Waheed A., Shah G.N., Tomatsu S., Sly W.S.:
RT "Human Egsyn Binds beta-Glucuronidase But Neither the Esterase Active
RT Site of Egsyn Nor the C-Terminus of beta-Glucuronidase Is Involved in
RT Their Interaction.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF177775; AD53175.1; -.
DR HSP; P21836; IWAH.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR KX Hydrolase.
SQ SEQUENCE 567 AA; 62448 MW; CC445067DC79EC59 CRC64;

Query Match 40.1%; Score 1248.5; DB 4; Length 567;
Best Local Similarity 44.7%; Pred. No. 2e-97;
Matches 248; Conservative 109; Mismatches 187; Indels 11; Gaps 8;

QY 36 LMAQTALGALHTKRPQV--TKYGTLOGK--QMHVGTPIQVFLGVPSPPGILRFAP 92
DB 11 LSAAGW--HPSSPPVVDVTHGKLVGKVLSEGFAPQVAFILGIFPAKPLGLRFTTP 68

QY 93 EPPEPWKGIKRDATYPPGCLQE--SWGQASMYVSTRERYKWLRFSDCLYLYNVAARAP 151
DB 69 QPAEPWSFKVNTSPYPMCTQDPKAGQLLSELFTNRKENIPKLSLSDCLYLYNITPADLT 128

QY 152 GDPQLPVMWFFPGAFIVGAASSYEGSDLAAREKVLVFLQHLRGLFGFLSTDDSHARGN 211
DB 129 KQRLPVMWTHGGGLVGAASVYDGLAALAHENVVVVTIYQRLGIVGFFSTGDEHSRG 188

QY 212 WGLDDQAAALRWQENIAAAGDPPGNVTLFGQAGAMSISGLMWSPLASGLPHRAISQSG 271
DB 189 WGHLDQVAALRWQDNIAAGDPPGNVTLFGQAGAMSISGLMWSPLASGLPHRAISQSG 248

QY 272 TALFRLFITSNPLK--VAKKVAHLACGNHNTQILVNCRLALSGTKVMRVSQKRFQLNLF 330
DB 249 VALTSVLVKGDDVXPLAEQIAITAGCKTTTSAVMVHCLQRKQTEBEELETTLKKMFLSLDL 308

QY 331 QRDPEEIIWMSPVVDGVIPDDPLVLLTQGVSSVYPYLLGVNMLEFNWLLP--YIMKFLP 389
DB 309 QGDPRSQPLGTVIDGMLLTKTEELQABRNFTVPMVGINQKQEPFGMLIPQMLMSYPL 368

QY 390 NRQAMRETTIKMLWSTRTLLNITKEQVPLVVEEYLDNVNHEHWMRLNRMMDIVODATF 449
DB 369 SEGQLDQKNTANSLWKSYPVLCIAKELIPEATEKYLGGTD--DTVKKKDLFLDLIADVMF 426

QY 450 VYATLQTAHYRDRDAGLPVLYEPEHH--ARGIIKVPRTDGDHGDHDEMFLFGGPAFLGLM 508
DB 427 GVPVSIVARNHRDAGAPTYMEFYQYRPSFSDMKPKTVIGDHGDELFSVFGAPFLKEGAS 486

QY 509 GKERALSQMKYKWFANPARTCNPDGNLPCWPRYNKDEKYLQIDFTTRVGKMLKEKNQAF 568
DB 487 EEEIRLSQMKYKWFANPARTCNPDGNLPCWPRYNKDEKYLQIDFTTRVGKMLKEKNQAF 546

QY 569 WWSLYSQORPEKQKQ 583
DB 547 WTNLFAKKAVEKPPQ 561
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RESULT 12
C35534
ID O35534 PRELIMINARY; PRT; 565 AA.
AC O35534;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.1).
GN CARBOXYLESTERASE.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus
OC Mesocricetus
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian Golden; TISSUE=Liver;
RA Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;
RT "Cloning and expression of a hamster liver cDNA encoding a novel
RT carboxylesterase which catalyzes the activation of carcinogenic
RT arylhydroxamic acids.";
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; D50578; BAA23604.1; -.
DR HSP; P21836; IWAH.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR KX Hydrolase; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 565 CARBOXYLESTERASE.
SQ SEQUENCE 565 AA; 62188 MW; 8273233A59DFIEDO CRC64;

Query Match 40.1%; Score 1247; DB 11; Length 565;
Best Local Similarity 42.7%; Pred. No. 2.7e-97;
Matches 240; Conservative 119; Mismatches 189; Indels 14; Gaps 8;

QY 26 WT--LCWLSLTCLMAQTALGALHTKRPQV--TKYGTLOGKQMHVG--KTPIQVFLGVPS 80
DB 2 WLYPLVW---ISLAACATWG--HPSSPPVVDVTHGKLVGKVLSEGFAPQVAFILGIVG 56

QY 81 RPPLGILRFAPPEPPEPWKGIKRDATYPPGCLQE--WGQASMYVSTRERYKWLRFSDCL 139
DB 57 KPPLGSLRFAPPEPPEPWKGIKRDATYPPGCLQE--WGQASMYVSTRERYKWLRFSDCL 116

QY 140 LYLNVYAPARAPGDPQLPVMWFFPGAFIVGAASSYEGSDLAAREKVLVFLQHLRGLFG 199
DB 117 LYLNTYTPADLTNKRSLPVMWTHGGGLVGAASVYDGLAALAHENVVVVTIYQRLGIVG 176

QY 200 FLSTDDSHARGNWGLDDQAAALRWQENIAAAGDPPGNVTLFGQAGAMSISGLMWSPLA 259
DB 177 FLSTGDEHSRGNWGLDDQAAALRWQENIAAAGDPPGNVTLFGQAGAMSISGLMWSPLA 236

QY 260 SGLFHRAISQSGTALFRLFITSNPLKVAHLACGNHNTQILVNCRLALSGTKVMRVS 319
DB 237 KNLFHRAISQSGVALTSALTFTKDAKPIAELVATLSGCKTTTSAVMVHCLQRKTEBELMET 296

QY 320 SNKMRFLQNLNFORDEEIIWMSPVVDGVIPDDPLVLLTQGVSSVYPYLLGVNMLEFNW 379
DB 297 SQKMLFLKLDLGNPKREYTPFLPTWIDGVFLSKSEEEILAEKSFNTVPMVGINQKQEGM 356

QY 380 LLPIYMKFPLNRQAMRETTIKMLWSTRTLLNITKEQVPLVVEEYLDNVNHEHWMRLN 439
DB 357 IIPMIMGYPLSEGLDQKNTANSLWKSYPVLCIAKELIPEATEKYLGGTD--KDL 414

QY 440 MMDIVODATFVYATLQTAHYRDRDAGLPVLYEPEHHARGII--VKPRTDGDHGDHDEM 498
DB 415 LLDLIADVIFGVPSVIVARNHRDAGAPTYMEFYRPSFSDMKPKTVIGDHGDELFSVFG 474
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Qy 499 GGFATGLSGVKGFEKALSLOMKMYKWFANFARTGNPNDGNLPCWPRYNKDEKYQLQDFTTRVG 555
Db 475 GSPFLXDGASEEINSLTKMFWFANFARNGNPNPGLPLHWPEYDQEGYMKIGASVQAA 534
Qy 559 MKLKEXKMAFWMSLYQSQRPEK 580
Db 535 HRLKDKEVIFWTELRAKEAER 556

RESULT 13
Q91ZV9 PRELIMINARY; PRT; 565 AA.
AC Q91ZV9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Triacylglycerol hydrolase [EC 3.1.1.1].
OS CES3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J; TISSUE=Liver;
RX MEDLINE=21363045; PubMed=11470237;
RA Dolinsky V.W., Sipione S., Lehner R., Vance D.E.;
RT "The cloning and expression of a murine triacylglycerol hydrolase cDNA
RT and the structure of its corresponding gene.";
RL Biochim. Biophys. Acta 1532:162-172(2001).
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF379751; AAX58067.1; -.
DR MGD; MGI:2148202; Ces3.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR InterPro; IPR002018; Carbesterase8.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; I.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 565 AA; 61887 MW; 1DAF99725721DF9A CRC64;

Query Match 40.0%; Score 1244.5; DB 11; Length 565;
Best Local Similarity 43.2%; Pred. No. 4.4e-97;
Matches 243; Conservative 117; Mismatches 181; Indels 21; Gaps 7;

Qy 28 LCWSLTCLMAQTALG-----ALHTRKRPVTVTKYGLQKQMHVGKTPIQVFLGVPSR 81
Db 6 LIW---LSLAACAWGYPSSPPVNTVKGVLGKYVNLGFTQ----PVAFLGVPEAK 57
Qy 82 PGLGILRAPPEPPKGIETATYPPGCLQES-WQLASMVSTREYKWLRESDCL 140
Db 58 PGLGSLRAPQPAEPFWFVNTISYPMGCSQDAVGVLSELTNRKENIPLOQSEDC 117
Qy 141 YLNYVAPARPGDPQLPVMVPPGAPIVGAASYSYGSDLAAREKVLVFLQHLGIFG 200
Db 118 YLNIYTPADLTNGRLPMVWVHGGGLVWGASTYDGLSALSAHENVVVTIQYRLGIWG 177
Qy 201 LSTDSDHARGNWGLDQWALRWQENIAFGDPGNVTLFGQSAGASISGLMWSPLAS 260
Db 178 FSTGDEHGRGNWGLDQWALRWQENIAFGDPGNVTLFGQSAGFSVSVLISPLAK 237
Qy 261 GLFHRAISQSGTALFLRFTISNPLKVAKKVAHLAGCNHNSTQILNCLREALSGTKMRS 320
Db 238 NLFHRAISGSGVSLTAALITTDVKPIAGLVATLSGCKTTTSAVMVHCLRQKTEDELLETS 297
Qy 321 NKMRFLQINFORDEEIIWMSPVQGVNIPDDPLVLLTGKQSVSVYLLGWNNLEFNWL 380
Db 298 LKNIPLKDLGLGNKPSYPPFLPTVIDGVVLVFKAPKEILAEEKSFSTVPIVGINKQEPGWI 357
Qy 361 LPYIMKFLPNQAKRKETITKMLWSTRTLLNITKEQVPLVWPEYLDNWNEDWKLNRM 440

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Db	358	IPTLMGYPLAEKGLDKQKANSULWWSKYPTTKISENMPVVAEBKYLGGTD--DJTKKKOLF	411		
Qy	441	MDIVQDQATVYATLQTAHVHRDAGLPVYLVEFEHHARGI-IVKPRITDGDADHGDGMYFLFG	499		
Db	416	QDLMDADVGVPSVIVSSSHDADAAGTYWFEYRPSFVSAMKPAVIGHGDEIFSVFG	475		
Qy	500	GPFATGLSGKEKALSLOMKYKWFANFARTGNPDGNLPCWPRYNKDEKYLQLDFTTRVGM	559		
Db	476	SPFLKDGASEETNLSSKVMKFWANFARNPNPAGGLPHWPEYDQEGYLKIGASTQAAQ	535		
Qy	560	KLKEKKMAFMSL--YOSQRP	578		
Db	536	RUKDKVSVFAELRAKESAQRP	557		
RESULT 14					
Q8VCT4	PRELIMINARY; PRT; 565 AA.				
ID	Q8VCT4				
AC	Q8VCT4;				
DT	01-MAR-2002 (TreeBLrel. 20, Created)				
DT	01-MAR-2002 (TreeBLrel. 20, Last sequence update)				
DT	01-OCT-2003 (TreeBLrel. 25, Last annotation update)				
DE	Carboxylesterase 3.				
GN	CES3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RA	Strausberg R.;				
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Colon;				
RX	MEDLINE=22354683; PubMed=12466851;				
RA	The FANTOM Consortium,				
RL	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RT	60,770 full-length cDNAs."				
RT	Nature 420:563-573 (2002).				
CC	1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.				
DR	EMBL; BC049198; AAH19198.1; -.				
DR	EMBL; AK078879; BAC37439.1; -.				
DR	MGD; MG1:2148202; Ces3.				
DR	GO; GO:0016787; F:hydrolase activity; IEA.				
DR	InterPro; IPR000379; Ser esters.				
DR	Pfam; PF00135; Coesterase_1.				
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.				
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.				
KW	Hydrolase.				
SQ	SEQUENCE 565 AA; 61787 MW; E85A9976F9916B34 CRC64;				
Query Match					
Best Local Similarity 40.0%; Score 1244.5; DB 11; Length 565;					
Matches 243; Conservative 117; Mismatches 181; Indels 21; Gaps 7;					
Qy	28	LCWSLTCLNQTALG-----ALHTRQVVTYKGTLOGKQMHVKGTPIQVFLGVPSR	81		
Db	6	LIW---LSLAACATWGPSPPVVNTVKGVLGKYNLEGFTQ-----PVAVFLGVPPAK	57		
Qy	82	PPLGILRFPAPPEPPKGRDATTYPGCLQES-WGQLASMYVSTRYKWLRFSSDCL	140		
Db	58	PPLSLRFPAPQAPKPSFVKNTTYPNCSQDAGVGQVLSLFTNRKNIPLQFSDCL	117		
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RESULT 15

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ID Q924V8 AC Q924V8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Carboxylesterase WH1 (EC 3.1.1.1).
GN CES3 OR CESMMH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, TISSUE=Liver;
RA Hosokawa M., Nakamura T., Nakata F., Takahashi D., Sakae M., Satoh T.,
RA Chiba K.;
RT "Purification, molecular cloning and expression of cDNA encoding
RT peroxisome proliferator inducible carboxylesterase isozymes from
RT C57BL/6 mouse liver."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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DR MGD; MGI:2148202; Ces3.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
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DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
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Query Match 39.9%; Score 1242.5; DB 11; Length 565;
Best Local Similarity 43.2%; Pred. No. 6.5e-97;
Matches 243; Conservative 117; Mismatches 181; Indels 21; Gaps 7;

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Search completed: August 3, 2004, 22:27:57

Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 09:15:47 ; Search time 6837.73 Seconds
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Title: US-10-001-227-3

Perfect score: 1752
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1752	100.0	1983	6	AX469746	Sequence	
3	1752	100.0	2081	6	AX377796	Sequence	
4	1356.4	77.4	2178	6	AX833215	Sequence	
5	1356.4	77.4	2178	9	AX094783	Homo sapi	
6	1059	60.4	2448	10	BC026374	Mus muscu	
7	957.8	54.7	2456	6	AX375990	Sequence	
8	957.8	54.7	2456	6	AX469751	Sequence	
9	957.8	54.7	2456	9	AX389504	Homo sapi	
10	902	51.5	2478	6	AX377795	Sequence	
11	601.16	34.3	1602	6	AX921060	Sequence	
12	434.4	24.8	1985	4	AB094147	Felis cat	
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17	427.2	24.4	1893	6	AB010633	Macaca fa	
18	426.2	24.3	1966	6	AX329628	Sequence	
19	426.2	24.3	1966	6	AX409500	Sequence	
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25	417.4	23.8	1918	10	RATCHES	Rattus norv	
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34	412.6	23.6	2141	6	AX401835	Sequence	
35	412.6	23.6	2141	10	RRSHVJL	Sequence	
36	411.6	23.5	1947	9	AY266104	Rattus no	
37	409.4	23.4	1839	10	L81114	Rattus norv	
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41	395	22.5	1953	10	BC019198	Mus muscu	
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ALIGNMENTS

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LOCUS	AX469748
DEFINITION	Sequence 3 from Patent WO244357.
ACCESSION	AX469748
VERSION	AX469748.1 GI:21901870
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Kapeller-Libermann,R. and Silos-Santiago,I..
TITLE	Methods of using 18903 to treat pain and pain-related disorders
JOURNAL	Patent: WO 0244357-A 3 06-JUN-2002;


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Db 1741 CAGAGCAATTC 1752

RESULT 2
AX469746
LOCUS AX469746 1983 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 1 from Patent WO0244357.
ACCESSION AX469746
VERSION AX469746.1 GI:21901868
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
Kapeller-Libermann,R. and Silos-Santiago,I.
TITILE Methods of using 18903 to treat pain and pain-related disorders
JOURNAL Patent: WO 0244357-A 1 06-JUN-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
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Db 1838 CAGAGGCAATTC 1849

RESULT 3
AX377796
LOCUS AX377796 2081 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 29 from Patent WO0212467.
ACCESSION AX377796
VERSION AX377796.1 GI:19573887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Baughn, M.R., Bruns, C.M., Das, D., Deleage, A.M., Ding, L.,
Elliot, V.S., Gandhi, A.R., Griffin, J.A., Hafalia, A.J., Khan, F.A.,
Lal, P., Lee, S., Lu, D.A., Lu, Y., Patterson, C., Ramkumar, J.,
Ring, H.Z., Sanjanwala, M.S., Tang, Y.T., Thornton, M. and
Tribouley, C.M.
Drug metabolizing enzymes
JOURNAL Patent: WO 0212467-A 29 14-FEB-2002;
Incyte Genomics, Inc. (US)
FEATURES
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1. 2081
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred No. 0;
Matches 1752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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LOCUS
DEFINITION Sequence 339 from Patent EP1347046.
ACCESSION AX833215
VERSION AX833215.1 GI:39919350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.
Full-length cDNA sequences
TITLE
JOURNAL Patent: EP 1347046-A 339 24-SEP-2003;
Research Association for Biotechnology (JRP)
FEATURES
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ORIGIN
Query Match 77.4%; Score 1356.4; DB 6; Length 2178;
Best Local Similarity 96.1%; Pred. No. 9.1e-281;
Matches 1423; Conservative 0; Mismatches 1; Indels 56; Gaps 1;
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QY 569 TTCTCGACACAGGCTCGGCATCTTCGGCTTCCTGA----- 604
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QY 605 -----GCACGGACGACAGCCACGCGCGCGGAA 445
Db 386 GACCGCAGCTGTGGCCAGAGCGGGGACTGGCACGGACGACAGCCACGCGCGCGGAA 632
QY 633 CTGGGGGCTGTGGACACAGATGGCGGCTCTGGCTGGGTGACAGAGACATCGACGCTT 692
Db 446 CTGGGGGCTGTGGACACAGATGGCGGCTCTGGCTGGGTGACAGAGACATCGACGCTT 505
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QY 753 AGGACTGATGATGTACCCCTAGCCCTCGGGTCTCTTCATCGGGGCATTTCCAGAGTGG 812
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QY 873 CCACCTGCTGGATGCAACCAACAGCACAGATCTGTGTAACTGCCTGAGGGCACT 932
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QY 1413 ATTTGAGCACCACGCTCGTGGAAATAATCGTCAAAACCCCGCACTGATGGGGCAGACCATGG 1472
Db 1226 ATTTGAGCACCACGCTCGTGGAAATAATCGTCAAAACCCCGCACTGATGGGGCAGACCATGG 1285
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Db 1286 GGATGAGATGACTTCCTCTTTGGGGCCCTTGGCCACAGGCGCTTCCATGGGTGAAGA 1345
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RESULT 5

AK094783

LOCUS

DEFINITION Homo sapiens cDNA FLJ37464 f1s, clone BRAWH2011795, weakly similar to LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1).

ACCESSION AK094783

VERSION AK094783.1 GI:21753911

KEYWORDS oligo capping; f1s (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M., Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2178)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 252-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - & 3' -end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

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/codon start=1

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ORIGIN

Query Match 77.4%; Score 1356.4; DB 9; Length 2178;

Best Local Similarity 96.1%; Pred. No. 9.1e-281;

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Qy 605 -----GCACGGACACAGCCACGCGCGCGCGGAA 632

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Qy 873 CCACCTGGCTGGATGCAAC 932

Db 686 CCACCTGGCTGGATGCAAC 745

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Qy 1113 TGTCAACACCTGGAATTCATTTGGCTTCTTGGCTTATATCATGAGTTCGGCTAACCCG 1172

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RESULT 6

LOCUS BC026374 2448 bp mRNA linear ROD 06-OCT-2003
 DEFINITION Mus musculus cDNA sequence BC026374, mRNA (cDNA clone MGC:31116
 IMAGE:4163362), complete cds.

VERSION BC026374.1 GI:20071335

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 2448)
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wegner, L., Shemen, C.W., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 2338257

PUBMED 12477932

REFERENCE 2 (bases 1 to 2448)

AUTHORS Srausberg, R.

TITLE
JOURNAL

Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 43 Row: c Column: 24
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22122766.

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ACCESSION AX375990
VERSION AX375990.1 GI:19170388
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
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Patent: WO 0168848-A 57 20-SEP-2001;
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ACCESSION AX377795
VERSION AX377795.1 GI:19573886
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Baughn, M.R., Bruns, C.M., Das, D., Deleage, A.M., Ding, L.,
Elliot, V.S., Gandhi, A.R., Griffin, J.A., Hafalia, A.J., Khan, F.A.,
Lai, P., Lee, S., Lu, D.A., Lu, Y., Patterson, C., Ramkumar, J.,
Ring, H.Z., Sanjanwalla, M.S., Tang, Y.T., Thornton, M. and
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TITLE Drug metabolizing enzymes
JOURNAL Patent: WO 0212467-A 28 14-FEB-2002;
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VERSION	AX921060.1 GI:40214762			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
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AUTHORS	Nov-x proteins and nucleic acids encoding same			
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RESULT 12
 AB094147
 LOCUS
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 ACCESSION AB094147
 VERSION AB094147.1 GI:30038512
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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 Miyazaki,M., Sai,H., Taira,H. and Yamashita,T.
 TITLE Molecular cloning of the feline liver carboxylesterase
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1985)
 Miyazaki,M., Sai,H., Taira,H. and Yamashita,T.
 TITLE Direct Submission
 AUTHORS Submitted (19-OCT-2002) Masao Miyazaki, Iwate University,
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 JOURNAL

FEATURES

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ACCESSION AB023629

VERSION AB023629.1 GI:14331124

KEYWORDS carboxylesterase D1; Dog liver carboxylesterase D1.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (sites)

AUTHORS Hosokawa,M., Suzuki,K., Takahashi,D., Mori,M., Satoh,T. and Chiba,K.

TITLE Purification, molecular cloning, and functional expression of dog liver microsomal acyl-CoA hydrolase: a member of the carboxylesterase multigene family

Arch. Biochem. Biophys. 389 (2), 245-253 (2001)

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REFERENCE 2 (bases 1 to 1923)

AUTHORS Hosokawa,M.

TITLE Direct Submission

JOURNAL Submitted (11-FEB-1999) Masakiyo Hosokawa, Chiba University, Faculty of Pharmaceutical Sciences, 1-33 Yayoi-cho, Chiba, Chiba 263-8522, Japan (E-mail:masakiyo@p.chiba-u.ac.jp, Tel:81-43-290-2921, Fax:81-43-290-2921)

FEATURES

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TITLE	Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257
MEDLINE	12477932
PUBMED	2 (bases 1 to 1975)
REFERENCE	Strausberg, R. Direct Submission Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gundaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louissegh, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
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